

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2005, 12:51:18 ; Search time 41 Seconds
(without alignments)
816.669 Million cell updates/sec

Title: us-10-713-208-6
Perfect score: 1800
Sequence: 1 MAEIGEDLDKSDVSSLIFLM.....ITESKDMHFSSLCILLDLVL 348
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79.*

1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	184.5	10.2	212	2 I67437	cysteine proteinas
2	184.5	10.2	277	2 S64710	cysteine proteinas
3	184.5	10.2	277	2 JC5410	CPP32 protein - mo
4	183.5	10.2	277	2 A55315	cysteine proteinas
5	180.5	10.0	452	2 JC6507	caspase-2 - rat
6	177.5	9.9	435	2 A54821	apoptosis regulato
7	169	9.4	312	2 B54821	ICE-LAP6 - human
8	161	8.9	416	2 G02635	interleukin-1-beta
9	149.5	8.3	182	2 I67436	interleukin-1-beta
10	138.5	7.7	418	2 B57511	interleukin-1-beta
11	136	7.6	383	2 A56084	interleukin-1-beta
12	134	7.4	454	2 JC7123	interleukin-1-beta
13	129.5	7.2	495	2 T20038	hypothetical prote
14	129.5	7.2	503	2 A49429	interleukin-1-beta
15	126.5	7.0	404	2 A42677	interleukin-1-beta
16	124.5	6.9	311	2 B56084	interleukin-1-beta
17	122	6.8	241	2 T30761	hypothetical prote
18	120	6.7	263	2 C56084	interleukin-1-beta
19	116	6.4	377	2 A57511	interleukin-1-beta
20	109.5	6.1	402	2 A46495	IL-1 beta converta
21	102	5.7	1537	2 F86509	conserved hypothec
22	102	5.7	1537	2 C81558	ct147 hypothethical
23	102	5.7	1537	2 H72112	assimilatory nitra
24	101.5	5.6	743	2 G83726	cag island protein
25	100	5.6	1819	2 A71928	oligodendrocytase
26	98.5	5.5	613	2 A99552	hypothetical zinc
27	98.5	5.5	680	2 T41670	early nodulin bind
28	98.5	5.5	1641	2 T10955	hypothetical prote
29	97.5	5.4	854	2 C83905	hypothetical prote

30 97.5 5.4 2104 2 T38774
31 97 5.4 892 2 AG1661
32 96.5 5.4 1287 2 T42658
33 96 5.3 488 2 T13385
34 95 5.3 892 2 A11289
35 95 5.3 1629 2 T06461
36 94.5 5.2 344 2 B70136
37 94 5.2 1713 2 A55347
38 94 5.2 2670 2 A46719
39 94 5.2 2671 2 A49873
40 94 5.2 4589 2 T14914
41 93.5 5.2 1811 2 T39252
42 93 5.2 455 2 G70113
43 93 5.2 1265 2 T47626
44 93 5.2 1875 2 S38173
45 93 5.2 1927 2 G64585

ALIGNMENTS

RESULT 1

I67437

cysteine proteinase (EC 3.4.22.-) P32 - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004

C:Accession: I67437

R:Flaws, J.A.; Kugu, K.; Trbovich, A.M.; DeSanti, A.; Tilly, K.I.; Hirshfield, A.N.; Tilly

Endocrinology 136, 5042-5053, 1995

A:Title: Interleukin-1-beta-converting enzyme-related proteases (IRPs) and mammalian cell

nulosa cells of the ovarian follicle.

A:Reference number: I53300; MUID:96042508; PMID:7588240

A:Accession: I67437

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-212 xRES>

A:Cross-references: UNIPROT:P55213; EMBL:U34685; NID:g1004370; PIDN:AAC52261.1; PID:g1004

C:Keywords: cysteine proteinase; hydrolase

Query Match 10.2%; Score 184.5; DB 2; Length 212;
Best Local Similarity 29.1%; Pred. No. 8.9e-07;
Matches 60; Conservative 36; Mismatches 81; Indels 29; Gaps 8;

QY 127 ERYKMKSLGICLIID-----CIGNTEL-----LRDTFSLGYEVOKFLHLSM 172
DB 5 DSSYKMDYPEMGLCIINNKFNKSTGSGARNGTDVDAANLRFTFMALKYEVKNKDLTR 64
QY 173 HGISQILGQFACMPHERDYDSFVCLVSRGSGSVYGVQTHSGLPLHHRMFMDGSCP 232
DB 65 EEIMELMDSVS-KEDHSKRSFVCLVSHGDEGVIFG---TNGFVCLKLTSFRRGYCR 120
QY 233 YLAGPKMFFFIQNYVVSQGLSDSSLLLEVDPGAMKNVEPKAKRGKGLCTVHREADFFWSLC 292
DB 121 SLTGKPLIIQ---ACRGTELDSG-IETDSCGDDV--ACQKKPV-----EADFLYAYS 169
QY 293 TADMSLLEQSHSPSLYLQCLSQKLR 318
DB 170 SAPGYVSWNSRGGSWFIQSLCAWLK 195

RESULT 2

S64710

cysteine proteinase (EC 3.4.22.-) CPP32 - Chinese hamster

C:Species: Crictetus griseus (Chinese hamster)

C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 05-Nov-1999

C:Accession: S64710; S72395

R:Wang, X.; Zelenksi, N.G.; Yang, J.; Sakai, J.; Brown, M.S.; Goldstein, J.L.

EMBO J. 15, 1012-1020, 1996

A:Title: Cleavage of sterol regulatory element binding proteins (SREBPs) by CPP32 during

A:Reference number: S64710; MUID:96183185; PMID:8605870

A:Accession: S64710

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A;Residues: 1-277 <WAN>
A;Cross-references: EMBL:U27463
R;Wang, X.
Submitted to the EMBL Data Library, May 1995
A;Reference number: S72395
A;Accession: S72395
A;Molecule type: mRNA
A;Residues: 1-79, 'A', '81-146, 'Y', '148-277 <WAW>
A;Cross-references: EMBL:U27463; NID:G1244443; PIDN:AAB01511.1; PID:G1244444
C;Keywords: apoptosis; cysteine proteinase; hydrolase

Query Match 10.2%; Score 184.5; DB 2; Length 277;
Best Local Similarity 27.9%; Pred. No. 1.3e-06;
Matches 67; Conservative 36; Mismatches 94; Indels 43; Gaps 9;

QY 96 KSLKPSNNFREPEPVKKS-IQSEAFLPQISPEERYKMKSKPLGLICLIID----- 144
DB 11 KSIK-----NFEVKTHGSKMSDGIYLDSS-----YKMDYPEMGVCIIINKNFKHKTGM 61
QY 145 --CIGNETEL--LRDTFTSLGYEVQKFLHLSMHGISOILGQFACMPHEHRDYSFVCLVLS 200
DB 62 TRPSGTVDAAKLRETFMNLKYEVRNKNDLTREEIVELM-KNASKEDHSEKRSFVCLVLS 120
QY 201 RGSQSVYGVQDTHSGPLPHIRRMFGSDSPYLAKPKMFFIQ--NYVVSQGLEDSLS 258
DB 121 HGDGVIQFTD---GPIDLKLTSPFRGDCRSLIGKPKLFIQACRGTELDGCIETDSG 177
QY 259 LEVDGPAMKNVEFKAQKRGCLTVHREADFFWSLCTADMSLLSEQSHSSPSLYLQCLSKLR 318
DB 178 TEDDMTCQK-----IPVEADFLYAYSTAPGYYSWRNPKDGSFWFIQSLCSMLK 224

RESULT 3
JC5410
C;Species: Mus musculus (house mouse)
C;Date: 10-Jun-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004
R;Mukasa, T.; Urabe, K.; Momoi, M.Y.; Kimura, I.; Momoi, T.
Biochem. Biophys. Res. Commun. 231, 770-774, 1997
A;Title: Specific expression of CPP32 in sensory neurons of mouse embryos and activation
A;Reference number: JC5410; MUID:97224429; PMID:9070890
A;Accession: JC5410
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-277 <MUK>
A;Cross-references: UNIPROT:P70677; DDBJ:D86352
A;Experimental source: embryo
C;Comment: This protein is involved in the apoptosis of dorsal root ganglia neurons.

Query Match 10.2%; Score 184.5; DB 2; Length 277;
Best Local Similarity 28.9%; Pred. No. 1.3e-06;
Matches 67; Conservative 35; Mismatches 93; Indels 37; Gaps 11;

QY 103 NNFREPEV--KKSIOSEAFLPQISPEERYKMKSKPLGLICLI-----DCIGN 148
DB 14 NNFVGKTIHGSKSV-DSGIYLDSS-----YKMDYPEMGICIIITNKNFKHKTGMSRSST 67
QY 149 ETEL--LRDTFTSLGYEVQKFLHLSMHGISOILGQFACMPHEHRDYSFVCLVSRGQSOS 206
DB 68 DVDAAANLRETFMGLKYEVRNKNDLTREEIMELMDSVS-KEDHSKRSSFVCLVLSHGDEGV 126
QY 207 VVGVDQTHSGPLPHIRRMFGSDSPYLAKPKMFFIQNYVVSQGLEDSLSLEVDGPAM 266
DB 127 IFG---TNGPVDLKKLTSPFRGDCYCSLTGKPKLFIQ---ACRGTELDGCIETDSGT- 178
QY 267 KNVEFKAQKRGCLTVHREADFFWSLCTADMSLLSEQSHSSPSLYLQCLSKLR 318
DB 179 -DEEMACQK-----IPVEADFLYAYSTAPGYYSWRNPKDGSFWFIQSLCSMLK 224

cysteine proteinase (EC 3.4.22.-) CPP32 precursor - human
N;Alternate names: cysteine proteinase CPP32
C;Species: Homo sapiens (man)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004
C;Accession: A55315; S58899; I39005
R;Fernandes-Alnemri, T.; Litwack, G.; Alnemri, E.S.
J. Biol. Chem. 269, 30761-30764, 1994
A;Title: CPP32, a novel human apoptotic protein with homology to Caenorhabditis elegans C-1
A;Reference number: A55315; MUID:95074098; PMID:7983002
A;Accession: A55315
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-277 <FER>
A;Cross-references: UNIPROT:P42574; GB:U13737; NID:G561665; PIDN:AAA65015.1; PID:G561666
R;Nicholson, D.W.; Ali, A.; Thornberry, N.A.; Vaillancourt, J.P.; Ding, C.K.; Gallant, M.
; Yu, V.L.; Miller, D.K.
Nature 376, 37-43, 1995
A;Title: Identification and inhibition of the ICE/CED-3 protease necessary for mammalian
A;Reference number: S58899; MUID:95319529; PMID:7596430
A;Accession: S58899
A;Molecule type: protein
A;Residues: 29-46;176-189, 'E', '191-193 <NIC>
R;Frewari, M.; Quan, L.T.; O'Rourke, K.; Deanovsers, S.; Zeng, Z.; Beidler, D.R.; Poirier,
Cell 81, 801-809, 1995
A;Title: Yama/CPP32 beta, a mammalian homolog of CED-3, is a CrmA-inhibitable protease t
A;Reference number: A56924; MUID:95292347; PMID:7774019
A;Accession: I39005
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-189, 'E', '191-277 <RES>
A;Cross-references: EMBL:U26943; NID:G857568; PIDN:AAA74929.1; PID:G857569
C;Keywords: apoptosis; cysteine proteinase; hydrolase; lymphocyte

Query Match 10.2%; Score 183.5; DB 2; Length 277;
Best Local Similarity 26.4%; Pred. No. 1.5e-06;
Matches 64; Conservative 41; Mismatches 100; Indels 37; Gaps 7;

QY 98 LKDPNNFREPEPVK----KSIQSEAFLPQISPEERYKMKSKPLGLICLIID----- 144
DB 1 MENTENSVDKSIKLEPKLIHGSSEMSDGSILDSNYKMDYPEMGLCIIINKNFKHKTG 60
QY 145 ---CIGNETEL--LRDTFTSLGYEVQKFLHLSMHGISOILGQFACMPHEHRDYSFVCLV 199
DB 61 MTSRSGTDVDAANLRETFMNLKYEVRNKNDLTREEIVELMRDVS-KEDHSKRSSFVCLV 119
QY 200 SRGQSQSVYGVQDTHSGPLPHIRRMFGSDSPYLAKPKMFFIQ--NYVVSQGLEDS 257
DB 120 SHGEGGIIFG---TNGPVDLKKLTNFRGDCRSLTGKPKLFIQACRGTELDGCIET 176
QY 258 LLEVDPGAMKNVEFKAQKRGCLTVHREADFFWSLCTADMSLLSEQSHSSPSLYLQCLSK 317
DB 177 GVDDDMACHK-----IPVDADFLYAYSTAPGYYSWRNPKDGSFWFIQSLCAML 223
QY 318 RQ 319
DB 224 KQ 225

RESULT 5
JC6507
C;Species: Rattus norvegicus (Norway rat)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: JC6507
R;Sato, N.; Milligan, C.E.; Uchiyama, Y.; Oppenheim, R.W.
Gene 202, 127-132, 1997
A;Title: Cloning and expression of the cDNA encoding rat caspase-2.
A;Reference number: JC6507; MUID:98087427; PMID:9427555
A;Accession: JC6507
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-452 <SAT>
A;Cross-references: UNIPROT:O55194; GB:U77933; NID:G2769705; PIDN:AAB96379.1; PID:G27697

Db 39 MIEDIQAGSGRRDQARQLIIDLETRGSA--LPLFISCLSDTQCDMLASFLRTNRQA 95
QY 79 VQAGAGSYRNVLAQAQKSLKOP-----SNNREEPVKKSIQSSSEAFPLPS 124
Db 96 GKLSKPTLENLTPTVLVRPIRPEVLRPTPRVDIGSGGFGDVGALSLRGN----- 148
QY 125 IPEERYKMKSKPLGICLIIDICIG--NETELLRDTFTSLGYEVQKFLHLSMHGISOILGQF 182
Db 149 -ADLAIVLSWPCGCHLIINNVCRESGLRTTGSNIDCEKLRFRFSLSHFVVEKGD 207
QY 183 A-----CMPHRDYDSFVCLVSRGSGSQS-----VYGVDTQTHSGLP--LHHI 222
Db 208 TAKKMWLALLEARQDHGALDCCVVILSHGCOASHLOPPGAVGYTD----GCPVSVEKI 263
QY 223 RRMFMGDCSPYLAGKPKMFIO-----NYVVSDDGLE-----SSLEVDG-PAMKV 269
Db 264 VNIIFNGTSCPSGGKPKLFFIQACGGEQKDHGFVASTSPEDSPSGNPEPATPPQGL 323
QY 270 EFKAQKRGGLCTVHREADFFWSLCTADMSLLEQSHSPSYLQCLSQKLRQ 319
Db 324 RIFDQLDAISSLTPSPDIFVSYSTFPFGFVSWRDPKSGSYVETLDDIFEQ 373
RESULT 9
I67436
interleukin-1-beta-converting enzyme and ced-3 homolog-1, long isoform - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C:Accession: I67436
R:Flaws, J.A.; Kugu, K.; Trbovich, A.M.; DeSanti, A.; Tilly, K.I.; Hirshfield, A.N.; Til
Endocrinology 136, 5042-5053, 1995
A:Title: Interleukin-1-beta-converting enzyme-related proteases (IRPs) and mammalian cel
nuloa cells of the ovarian follicle.
A:Reference number: I53300; MUID:96042508; PMID:7588240
A:Accession: I67436
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-182 <RES>
A:Cross-references: UNIPROT:P55215; EMBL:U34684; NID:g1004368; PIDN:AAC52260.1; PID:g100

Query Match 8.3%; Score 149.5; DB 2; Length 182;
Best Local Similarity 31.0%; Pred. No. 0.00033;
Matches 44; Conservative 18; Mismatches 61; Indels 19; Gaps 4;
QY 136 PLGICLIIDCI-----GNETE--LLRDTFTSLGYEVQKFLHLSMHGISOILGQ 181
Db 1 PGLALVMSNVHPTGKDLFRSGGDVHTTLVTLFKLGINVHVLYDQTAQEMQEKLN 60
QY 182 FACMPHRDYDSFVCLVSRGSGSQSYGVVDQTHSGLPFLHHRMFMGDCSPYLAGKPKMF 241
Db 61 FAQLPAHRYTDSICVALLSHGVEGGYGVDD--GKLLQLQEVFLFDNANCPSLQNKPKMF 118
QY 242 FQNYVVSQGLEDDSSLEVDG 263
Db 119 FIQ---ACRGDETRDGVDDQDG 137
RESULT 10
B57511
interleukin-1 beta converting enzyme (EC 3.4.22.-) ICErel-III - human
C:Species: Homo sapiens (man)
C:Date: 08-Dec-1995 #sequence_revision 08-Dec-1995 #text_change 09-Jul-2004
C:Accession: B57511; S62183
R:Munday, N.A.; Vaillancourt, J.P.; Ali, A.; Casano, F.J.; Miller, D.K.; Molineaux, S.M.
J. Biol. Chem. 270, 15870-15876, 1995
A:Title: Molecular cloning and pro-apoptotic activity of ICE-relIII and ICE-relIII, membe
A:Reference number: A57511; MUID:95318183; PMID:7797592
A:Accession: B57511
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-418 <MUN>
A:Cross-references: UNIPROT:P51878; GB:U28015; NID:g975300; PIDN:AAA5172.1; PID:g90393d

R:Faucheu, C.; Blanchet, A.M.; Collard-Dutilleul, V.; Lalanne, J.L.; Diu-Hercend, A.
Eur. J. Biochem. 236, 207-213, 1996
A:Title: Identification of a cysteine protease closely related to interleukin-1-beta-con
A:Reference number: S62183; MUID:96184899; PMID:8617266
A:Accession: S62183
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 55-317, 'L', 319-418 <FAU>
A:Cross-references: EMBL:X94993; NID:g1155085; PIDN:CAA64450.1; PID:g1155086
C:Keywords: cysteine proteinase; hydrolase

Query Match 7.7%; Score 138.5; DB 2; Length 418;
Best Local Similarity 23.4%; Pred. No. 0.0069;
Matches 77; Conservative 52; Mismatches 125; Indels 75; Gaps 16;

QY 10 KSDVSSLIPLMKD-----YMGRG-----KISKEKSFLLDLVLEKLNLVAPDQDLLE 57
Db 50 KTVKMLGYLGDVHGVFNVLAKHDVITLKEEEKKKYDAKIEDKALILV-----DSL 104
QY 58 KCLKNHRIIDLTKIQKYKQSVQAGTSYRNVLAQAIOKSLKDPNNF-----REBPVKK 112
Db 105 K-NRVAHQMFQT--LLNWDQKI-----TSVKPLLOIEAGPPESAESTNLIKCPREFLRL 158
QY 113 SIQSEAFPLQSIPEERYKMKSKPLGICLI-----DCIGNETELLRT 156
Db 159 CKKNHDEIVPIKKREDRRR-----LALIICNTKFDHLPARGAHYDIVG-----MKRL 206
QY 157 FTSLSGVEQKFLHLSMHGISOILGOFACMPHERDVSFVCLVSRGSGSQSYGV--DQT 213
Db 207 LGLGYTVVDEKNLTARDMESVLRAPARPEKHSDDSTFLVLMSHGILEGICGTAHKKKK 266
QY 214 HSGPLHHRMFMGDCSPYLAGKPKMFQIYVVSQDQ-----LEDS--SLLEVDGPA 265
Db 267 PDVLVYDITFIQFNRRNCLSLKDKPKVLIQV---ACRGEKHGELVWRDSPASLAVISSQS 323
QY 266 MNVEFKAKQKRGCLTVHREADFFWSLCTA 294
Db 324 SENLEADS-----VCKIHBEKDFI-AFCSS 347

RESULT 11
A56084
interleukin-1beta converting enzyme beta isozyme - human
C:Species: Homo sapiens (man)
C:Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 09-Jul-2004
C:Accession: A56084
R:Alnemri, E.S.; Fernandes-Alnemri, T.; Litwack, G.
J. Biol. Chem. 270, 4312-4317, 1995
A:Title: Cloning and expression of four novel isoforms of human interleukin-1beta convert
A:Reference number: A56084; MUID:95181414; PMID:7876192
A:Accession: A56084
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-383 <ALN>
A:Cross-references: UNIPROT:P29466; GB:U13697; NID:g717039; PIDN:AAC50107.1; PID:g717040
C:Genetics:
A:Gene: IL1BCE
C:Keywords: alternative splicing

Query Match 7.6%; Score 136; DB 2; Length 383;
Best Local Similarity 24.0%; Pred. No. 0.0095;
Matches 81; Conservative 54; Mismatches 145; Indels 58; Gaps 12;

QY 24 MCRGKISKEKSFLLDLVLEKLNLVAPDQDLLEKCLKNHRIIDLTKIQKYKQSVQ--- 80
Db 17 MEGGTIN---GLDSELTQTRVLNKEEMKVKRENATVMDKTALIDSVIPKGAQACI 73
QY 81 -----GAGTSYRNVLAQAIOKSLKDPNNFPEEPVKK-SIQSEAFPLQSIPEERY 130
Db 74 TYICEEDSVIAGTGLGSAAPQVQDNPAFPTSSGSEGNVKLCSLEEAQIRWKQSAEIVP 133
QY 131 KM-KSKPLGICLI-----DCI-----GNETELLRT--FTSLGYEVQKFLHLSMHGISOI 178

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Db 134 IMDKSSRLALICNEEPDSIPRTGAEDVITGMTMLLQNLGYSVDVKKNLTSADWTE 193
QY 179 LQOFACWPEHRDVSFVCLVSRGGSQSVG---VDQTHSGLPLHHRMFMGDSCPYLA 235
Db 194 LEAFARPEHKTSDFLVFMSHGIREGICKHSEQVDPDILQNAIFNMLANTKNCPSLK 253
QY 236 GKPKMFQIO-----NYVSDGOLEDSSILEVDGPAKKNVEFKAQRGLCTVH 282
Db 254 DRPKVILIIQACRGDSGVVWFKDSVGSNLSLPTTEEFEDDAIKK-----AH 301
QY 283 READFFWLSCTADMSLLEQSH--SSPSLYLQCLSKQLRQ 319
Db 302 IEKDFI-AFCSSPDNVSMRHPTMGSVFGRLEHMQE 338

RESULT 12
JC7123
C:Species: Mus musculus (house mouse)
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C:Accession: JC7123
R:Fujita, E.; Jinbo, A.; Maturaki, H.; Konishi, H.; Kikkawa, U.; Momoi, T.
Biochem. Biophys. Res. Commun. 264, 550-555; 1999
A:Title: Akt phosphorylation site found in human caspase-9 is absent in mouse caspase-9.
A:Reference number: JC7123; MUID:20001956; PMID:10529400
A:Accession: JC7123
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-454 <FUJ>
A:Cross-references: UNIPROT:Q9R0T0; DDBJ:AB019600; NID:G6440941; PID:G6440942

Query Match 7.4%; Score 134; DB 2; Length 454;
Best Local Similarity 33.1%; Pred. No. 0.017;
Matches 45; Conservative 15; Mismatches 52; Indels 24; Gaps 6;

QY 130 YKMKSPKLGICLIID----C-----IGNET-----ELLRDTFTSLGVEQKFLHLSMHGI 175
Db 191 YTLDSOPCGHCLLIINNPNCRSGLGTRTGSNIDRKLEHRFWLRFMVEVKNDLTAKKM 250
QY 176 SQILGQFACWPEHRDVSFVCLVSRGGSQ-----YGVQDQTHSGGLPLHHRMFMG 228
Db 251 VTALMEMA-HRNHRALDCFVVVILSHGQASHQFPFCVVGTD--GCSVSIKIVNIFNG 307
QY 229 DSCPYLAKPKMFFIQ 244
Db 308 SGCPSLGGKPKLFFIQ 323

RESULT 13
T20038
hypothetical protein C48D1.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T20038
R:Burton, J.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z19214
A:Accession: T20038
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-495 <WIL>
A:Cross-references: EMBL:Z81049; PIDN:CAB02848.1; GSPDB:GN00022; CESP:C48D1.2
A:Experimental source: clone C48D1
C:Genetics:
A:Gene: CESP:C48D1.2
A:Map position: 4
A:Introns: 44/3; 93/2; 178/1; 288/3; 360/1; 402/3; 466/1

Query Match 7.2%; Score 129.5; DB 2; Length 495;
Best Local Similarity 24.0%; Pred. No. 0.042;
Matches 63; Conservative 37; Mismatches 86; Indels 77; Gaps 12;

QY 70 TKIQKYQSVQAGTGYRNVLQAAIQKS-----LKDPNNFREEP----- 109
Db 126 TRVHRDSVSSVSFTSYQDIYSRRSRSRALHSSDRHNSPPVNAFPSPSSANSF 185
QY 110 -----VKKSIQSEAFLPQSIPEE-----RYKMKSKPLGIC 140
Db 186 TCGSSIGYSSRRNSRFSKASGPTQYIFHEEDMNFVDAPTISRVDKTYRNFSSPRGMC 245
QY 141 LIID-----CIGNETELLRDTFTSL-----GYEVQKFLHLSMHGISQILGQFACWPEHR 189
Db 246 LIINNEHFQMPTRNGTKADKONLTNLFRCMGYTVICKONLTGRGMLLTIRDAFA---KHE 302
QY 190 DY-DSFVCLVSRGGSQSVYGVQDTHSGGLPL--HHIRRMFMGDSQVCLAGKPKMFFIQNY 246
Db 303 SHGDSAILVILSHGENVIIGVDD----IPISTHEIYDLNANAPRLANKPKIVFQV-- 356
QY 247 VVSDGOLEDSS---LLEVDG-PA 265
Db 357 -ACRGERRDNGFPVLDSVDGVPA 378

RESULT 15
A42677
interleukin-1 beta converting enzyme (EC 3.4.22.-) - human
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Db 125 TRVHRDSVSSVSFTSYQDIYSRRSRSRALHSSDRHNSPPVNAFPSPSSANSF 184
QY 110 -----VKKSIQSEAFLPQSIPEE-----RYKMKSKPLGIC 140
Db 185 TCGSSIGYSSRRNSRFSKASGPTQYIFHEEDMNFVDAPTISRVDKTYRNFSSPRGMC 244
QY 141 LIID-----CIGNETELLRDTFTSL-----GYEVQKFLHLSMHGISQILGQFACWPEHR 189
Db 245 LIINNEHFQMPTRNGTKADKONLTNLFRCMGYTVICKONLTGRGMLLTIRDAFA---KHE 301
QY 190 DY-DSFVCLVSRGGSQSVYGVQDTHSGGLPL--HHIRRMFMGDSQVCLAGKPKMFFIQNY 246
Db 302 SHGDSAILVILSHGENVIIGVDD----IPISTHEIYDLNANAPRLANKPKIVFQV-- 355
QY 247 VVSDGOLEDSS---LLEVDG-PA 265
Db 356 -ACRGERRDNGFPVLDSVDGVPA 377

RESULT 14
A49429
interleukin-1 beta-converting enzyme homolog CED-3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A49429; T37312
R:Yuan, J.; Shaham, S.; Ledoux, S.; Ellis, H.M.; Horvitz, H.R.
Cell 75, 641-652, 1993
A:Title: The C. elegans cell death gene ced-3 encodes a protein similar to mammalian inter-
A:Reference number: A49429; MUID:94061982; PMID:8242740
A:Accession: A49429
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-503 <YUA>
A:Cross-references: UNIPROT:P42573; GB:L29052; NID:G6503232; PIDN:AAA27982.2; PID:G65032.2
A>Note: sequence extracted from NCBI backbone (NCBIN:139825, NCBI:P:139826)
A:Accession: T37312
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-417,'R',419-503 <YU2>
A:Cross-references: EMBL:L29052; PIDN:AAA27982.1
C:Genetics:
A:Gene: ced-3
A:Introns: 45/3; 94/2; 179/1; 289/3; 361/1; 403/3; 483/3

Query Match 7.2%; Score 129.5; DB 2; Length 503;
Best Local Similarity 24.0%; Pred. No. 0.043;
Matches 63; Conservative 37; Mismatches 86; Indels 77; Gaps 12;

QY 70 TKIQKYQSVQAGTGYRNVLQAAIQKS-----LKDPNNFREEP----- 109
Db 126 TRVHRDSVSSVSFTSYQDIYSRRSRSRALHSSDRHNSPPVNAFPSPSSANSF 185
QY 110 -----VKKSIQSEAFLPQSIPEE-----RYKMKSKPLGIC 140
Db 186 TCGSSIGYSSRRNSRFSKASGPTQYIFHEEDMNFVDAPTISRVDKTYRNFSSPRGMC 245
QY 141 LIID-----CIGNETELLRDTFTSL-----GYEVQKFLHLSMHGISQILGQFACWPEHR 189
Db 246 LIINNEHFQMPTRNGTKADKONLTNLFRCMGYTVICKONLTGRGMLLTIRDAFA---KHE 302
QY 190 DY-DSFVCLVSRGGSQSVYGVQDTHSGGLPL--HHIRRMFMGDSQVCLAGKPKMFFIQNY 246
Db 303 SHGDSAILVILSHGENVIIGVDD----IPISTHEIYDLNANAPRLANKPKIVFQV-- 356
QY 247 VVSDGOLEDSS---LLEVDG-PA 265
Db 357 -ACRGERRDNGFPVLDSVDGVPA 378

RESULT 15
A42677
interleukin-1 beta converting enzyme (EC 3.4.22.-) - human
```

C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: A54263; A42677; S21734; S24164
R:Cerretti, D.P.; Hollingsworth, L.T.; Kozlosky, C.J.; Valentine, M.B.; Shapiro, D.N.; M
Genomics 20, 468-473, 1994
A:Title: Molecular characterization of the gene for human interleukin-lbета converting e
A:Reference number: A54263; MUID:94307734; PMID:8034320
A:Accession: A54263
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-404 <CE2>
A:Cross-references: UNIPROT:P29466; GB:I27475
R:Cerretti, D.P.; Kozlosky, C.J.; Mosley, B.; Nelson, N.; Van Ness, K.; Greenstreet, T.A
Science 256, 97-100, 1992
A:Title: Molecular cloning of the interleukin-lbета converting enzyme.
A:Reference number: A42677; MUID:92229430; PMID:1373520
A:Accession: A42677
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-404 <CER>
A:Cross-references: GB:M87507; NID:9435598; PIDN:AAA66942.1; PID:g186286
R:Thornberry, N.A.; Bull, H.G.; Calaycay, J.R.; Chapman, K.T.; Howard, A.D.; Koestura, M.
J.; Ding, G.J.F.; Egger, L.A.; Gaffney, E.P.; Limjuco, G.; Palyha, O.C.; Raju, S.M.; Rol
cci, M.J.
Nature 356, 768-774, 1992
A:Title: A novel heterodimeric cysteine protease is required for interleukin-lbета proce
A:Reference number: S21734; MUID:92244338; PMID:1574116
A:Accession: S21734
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-404 <THO>
A:Cross-references: EMBL:X65019; NID:g33792; PIDN:CAA46153.1; PID:g33793
R:Kronheim, S.R.; Muma, A.; Greenstreet, T.; Glackin, P.J.; van Ness, K.; March, C.J.;
Arch. Biochem. Biophys. 296, 698-703, 1992
A:Title: Purification of interleukin-lbета converting enzyme, the protease that cleaves
A:Reference number: S24164; MUID:92337439; PMID:1321594
A:Accession: S24164
A:Status: preliminary
A:Molecule type: protein
A:Residues: 120-135, 'AX', 138-139, 'X', 141-142 <KRO>
C:Genetics:
A:Gene: GDB:IL1BC
A:Cross-references: GDB:132368; OMIM:147678
A:Map position: 11q23-11q23
C:Keywords: cysteine proteinase; hydrolase

Query Match 7.0%; Score 126.5; DB 2; Length 404;
Best Local Similarity 23.1%; Pred. No. 0.054;
Matches 83; Conservative 56; Mismatches 141; Indels 79; Gaps 14;

QY 24 MGRGKISKESFLDLVVELEKLNVLAPDQDLLEKCLKNHRIIDLTKIKYKQSVQ--- 80
DB 17 MGEETIN---GLLDELLOTRVLNKEEMKVKRENATVMDKTRALIDSVIPKGAQACIQCI 73
QY 81 -----GAGT-----SYRNVLOA-----AIQSKLDPSNNFREPV 110
DB 74 TYICEEDSYLAGTGLGLSADQTSGLYNMQDSQGLSFPAPQAVQDNPAIMPSTSSGSEGNV 133
QY 111 KK-SIOESEAFLPOSIPERYKM-KSKPLGICLI-----DCI-----GNETELLRDT--F 157
DB 134 KLCSEEAQRIRWKQKGAETYPIMDKSRTRLALIIINEEFDSIPRRTGAEVDITGMTMLL 193
QY 158 TSLGYEVQKFLHLSMHGISQILQGFACMPHEHRYDSFVCLVSRGGSQSVYG---VDQTH 214
DB 194 QNLGYSVDVKKNLTASDMTELEAFAPRPHKTSDFLVLVFNHSHGREGICGKKHSEQVP 253
QY 215 SGLPLHHIRRMFGDSCPYLAGKPKMFFIQ-----NYVVSQGLDSSLLEV 261
DB 254 DILQLNAIFNMLNTKNCPSLKDKPKVIIQACRGSDPGVWVFKDSVGVSGNLSLPTTEEF 313
QY 262 DGPAMKRVFKAKRGKLCVTHREADFWSLCTADMSLLEQSH--SSPSLYLQCLSQKLQ 319
DB 314 EDDAIKK-----AHIEKDFI-AFCSSTPDNVSWRHFTMGSVFGRLEHMQE 359

Search completed: June 20, 2005, 13:06:07
Job time : 44 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2005, 12:50:04 ; Search time 174 Seconds
(without alignments)
1024.158 Million cell updates/sec

Title: US-10-713-208-6
Perfect score: 1800
Sequence: 1 MAEIGEDLDKSDVSSLIPLM.....ITSEKDMHFFSLGICILLVDL 348

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 03:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1635	90.8	480	1 CFLA HUMAN	O15519 h casp8 and
2	1208	67.1	487	2 O6QN97	O6qn97 sus scrofa
3	1018	56.6	481	2 O812G4	O812g4 mus musculus
4	1006.5	55.9	484	1 CFLA MOUSE	O35732 m casp8 and
5	600	33.3	497	2 O6NTR7	O6ntr7 xenopus lae
6	471	26.2	418	2 O8UVG5	O8uvgs brachydanio
7	403.5	22.4	219	2 O6QN98	O6qn98 sus scrofa
8	345	19.2	218	2 O99MZ5	O99mz5 rattus norv
9	318.5	17.7	482	2 O9JHX4	O9jhx4 rattus norv
10	313	17.4	479	1 ICES HUMAN	O14790 h caspase-8
11	302.5	16.8	482	2 O90WU1	O90wu1 gallus gall
12	297	16.5	480	1 ICES MOUSE	O89110 mus musculus
13	277	15.4	78	2 O8MJ18	O8mj18 macaca mula
14	270	15.0	512	2 O6PAD9	O6pad9 xenopus lae
15	267	14.8	520	2 O9IB62	O9ib62 xenopus lae
16	265.5	14.8	476	2 O66119	O66119 brachydanio
17	265.5	14.8	476	2 O9IB73	O9ib73 brachydanio
18	248.5	13.8	521	1 ICES HUMAN	O92851 homo sapien
19	248.5	13.8	522	2 O8IU05	O8iup5 homo sapien
20	244	13.6	478	2 O6KF62	O6kf62 homo sapien
21	235	13.1	455	2 O6KF63	O6kf63 homo sapien
22	233	12.9	500	2 O9IB64	O9ib64 xenopus lae
23	233	12.9	283	2 O93417	O93417 gallus gall
24	213	11.8	366	2 O6ESN8	O6esn8 ictalurus p
25	210.5	11.7	496	2 O81749	O81749 suberites d
26	199	11.1	293	1 ICES HUMAN	P55212 homo sapien
27	199	11.1	303	2 O9IB66	O9ib66 xenopus lae
28	198.5	11.0	400	2 O8ITP2	O8itp2 brachydanio
29	195.5	10.9	424	1 ICES2 CHICK	O98943 gallus gall
30	193.5	10.8	277	1 ICES3_PIG	O95nd5 sus scrofa
31	192.5	10.7	318	2 O9IB65	O9ib65 xenopus lae

32	192	10.7	277	1 ICES CANFA	O8mtk5 canis famil
33	190.5	10.6	317	2 O6DCI2	O6dc12 xenopus lae
34	190	10.6	328	2 O8ITP3	O8itp3 brachydanio
35	189.5	10.5	277	1 ICES3_FELCA	O8mjul felis silve
36	188.5	10.5	277	1 ICES3_MOUSE	P70677 mus musculus
37	187.5	10.4	302	2 O918S9	O918s9 oncorhynch
38	186.5	10.4	280	2 O8JIS9	O8jis9 oryzias lat
39	185.5	10.3	277	1 ICES3_RAT	P55213 rattus norv
40	185.5	10.3	282	1 ICES3_XENLA	P55866 xenopus lae
41	184.5	10.2	182	2 O77623	O77623 ovis aries
42	184	10.2	290	2 O8JIS8	O8jis8 oryzias lat
43	183.5	10.2	277	1 ICES3_CRILO	O60431 cricetus lat
44	183.5	10.2	277	1 ICES3_HUMAN	P42574 homo sapien
45	182.5	10.1	277	2 O6JH80	O6jhr80 cricetus lat

ALIGNMENTS

RESULT 1

ID	CFLA_HUMAN	STANDARD	PRT	480 AA
AC	O15519; O14673; O14674; O14675; O15137; O15138; O15356; O15510; O43618; O43619; O43620; O60458; O60459; O96TB4; Q9UEW1;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	CASP8 and FADD-like apoptosis regulator precursor (Cellular FLICE-like inhibitory protein) (c-FLIP) (Caspase-eight-related protein) (Casper)			
DE	(Caspase-like apoptosis regulatory protein) (CLARP) (MACH-related inducer of toxicity) (MRIT) (Caspase homolog) (CASH) (inhibitor of FLICE) (i-FLICE) (FADD-like antiapoptotic molecule 1) (Flame-1) (Usurpin)			
DE	Names=CFLAR; Synonyms=CASH, CLARP, MRIT;			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORMS 1; 13 AND 14), AND MUTAGENESIS OF TYR-360.			
RC	TISSUE=Embryonic kidney, and Umbilical vein endothelial cells;			
RX	MEDLINE=97352452; PubMed=9208847; DOI=10.1016/S1074-7613(00)80450-1;			
RA	Shu H.-B., Halpin D.R., Goeddel D.V.;			
RL	"Casper is a FADD- and caspase-related inducer of apoptosis.";			
IM	Immunity 6:751-763(1997).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).			
RX	MEDLINE=97470967; PubMed=9326610; DOI=10.1073/pnas.94.21.11333;			
RA	Han D.K.M., Chaudhary P.M., Wright M.E., Friedman C., Frask B.J., Riedel R.T., Baskin D.G., Schwartz S.M., Hood L.;			
RA	"MRIT, a novel death-effector domain-containing protein, interacts with caspases and BclXL and initiates cell death.";			
RT	Proc. Natl. Acad. Sci. U.S.A. 94:11333-11338(1997).			
RL	[3]			
RN	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).			
RP	TISSUE=Periphera blood lymphocytes;			
RC	MEDLINE=97373543; PubMed=9217161; DOI=10.1038/40657;			
RX	MEDLINE=97360133; PubMed=9217161; DOI=10.1038/40657;			
RA	Imbler M., Thome M., Hahne M., Schneider P., Hofmann K., Steiner V., Bodmer J.-L., Schroeter M., Burns K., Mattmann C., Rimoldi D., French J.E., Tschopp J.;			
RA	"Inhibition of death receptor signals by cellular FLIP.";			
RL	Nature 388:190-195(1997).			
RN	[4]			
RP	SEQUENCE FROM N.A. (ISOFORMS 1; 8; 9 AND 10), AND MUTAGENESIS OF ASP-376.			
RC	TISSUE=T-cell;			
RX	MEDLINE=97373543; PubMed=9228018; DOI=10.1074/jbc.272.30.19542;			
RA	Srinivasula S.M., Ahmad M., Oltie S., Bullrich F., Banks S., Wang Y., Fernandes-Alnemri T., Croce C.M., Litwack G., Tomaselli K.J., Armstrong R.C., Alnemri E.S.;			
RA	"FLAME-1, a novel FADD-like anti-apoptotic molecule that regulates Fas/TNFR1-induced apoptosis.";			
RT				

RL	J. Biol. Chem. 272:18542-18545(1997).	RT	"Generation and initial analysis of more than 15,000 full-length human
RN	[5]	RL	and mouse cDNA sequences.";
RP	SEQUENCE FROM N.A. (ISOFORM 1).	RN	[12]
RC	TISSUE=Umbilical vein endothelial cells;	RP	MEDLINE=9909897; PubMed=9889531;
RX	MEDLINE=97362203; PubMed=9211860; DOI=10.1074/jbc.272.28.17255;	RX	Scaffidi C., Schmitz I., Krammer P.H., Peter M.E.;
RA	Hu S., Vincenz C., Ni J., Gentz R., Dixit V.M.;	RA	"The role of c-FLIP in modulation of CD95-induced apoptosis.";
RT	"I-FLICE, a novel inhibitor of tumor necrosis factor receptor-1- and	RL	J. Biol. Chem. 274:1541-1548(1999).
RL	CD-95-induced apoptosis.";	RN	[13]
RN	J. Biol. Chem. 272:17255-17257(1997).	RP	INDUCTION.
RP	SEQUENCE FROM N.A. (ISOFORMS 4; 5; 6 AND 7).	RX	MEDLINE=99244884; PubMed=10227994;
RA	Hu S., Dixit V.M.;	RA	Algeciras-Schmich A., Griffith T.S., Lynch D.H., Paya C.V.;
RL	Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.	RT	"Cell cycle-dependent regulation of FLIP levels and susceptibility to
RN	[7]	RT	Fas-mediated apoptosis.";
RP	SEQUENCE FROM N.A. (ISOFORMS 1; 11 AND 12).	RL	J. Immunol. 162:5205-5211(1999).
RC	TISSUE=Kidney;	RN	[14]
RX	MEDLINE=99218584; PubMed=10200473;	RP	SPLICE ISOFORM(S) THAT ARE POTENTIAL NMD TARGET(S).
RA	Rasper D.M., Vaillancourt J.P., Hadano S., Houtzager V.M., Seiden I.,	RX	PubMed=14759258; DOI=10.1186/gb-2004-5-2-r8;
RA	Keen S.L.C., Tawa P., Xanthoudakis S., Nasir J., Martindale D.,	RA	Hillman R.T., Green R.E., Brenner S.E.;
RA	Koop B.F., Peterson E.P., Thornberry N.A., Huang J., MacPherson D.P.,	RA	"An unappreciated role for RNA surveillance.";
RA	Black S.C., Hornung F., Lenardo M.J., Hayden M.R., Roy S.,	RL	Genome Biol. 5:RESEARCH008.16(2004).
RA	Nicholson D.W.;	CC	!- FUNCTION: Apoptosis regulator protein which may function as a
RT	"Cell death attenuation by 'Usurpin', a mammalian DED-caspase	CC	crucial link between cell survival and cell death pathways in
RT	homologue that precedes caspase-8 recruitment and activation by the	CC	mammalian cells. Acts as an inhibitor of TNFRSF6 mediated
RT	CD-95 (Fas, APO-1) receptor complex.";	CC	apoptosis. A proteolytic fragment (p43) is likely retained in the
RL	Cell Death Differ. 5:271-288(1998).	CC	death-inducing signaling complex (DISC) thereby blocking further
RN	[8]	CC	recruitment and processing of caspase-8 at the complex. Full
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).	CC	length and shorter isoforms have been shown either to induce
RX	TISSUE=skin fibroblast;	CC	apoptosis or to reduce TNFRSF-triggered apoptosis. Lacks enzymatic
RC	MEDLINE=97426025; PubMed=9289491; DOI=10.1074/jbc.272.32.19641;	CC	(caspase) activity.
RA	Goltsev Y.V., Kovalenko A.V., Arnold E., Varfolomeev E.E.,	CC	!- SUBUNIT: TNFRSF6 stimulation triggers recruitment to the death-
RA	Brodianskii V.M., Wallach D.;	CC	inducing signaling complex (DISC) formed by TNFRSF6, FADD and
RT	"CASH, a novel caspase homologue with death effector domains.";	CC	caspase-8. A proteolytic fragment (p43) stays associated with the
RL	J. Biol. Chem. 272:19641-19644(1997).	CC	DISC. Also interacts with caspase-10, caspase-3, TRAF1, TRAF2 and
RN	[9]	CC	Bcl-X(L) (in vitro).
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).	CC	!- ALTERNATIVE PRODUCTS:
RC	TISSUE=Colon carcinoma;	CC	Event=Alternative splicing; Named isoforms=14;
RX	MEDLINE=98021435; PubMed=9380701; DOI=10.1073/pnas.94.20.10717;	CC	Name=1; Synonyms=FLIP-L, CLARP1, MRIT alpha-1, CASH alpha, I-FLICE
RA	Inohara N., Koseki T., Hu Y., Chen S., Nunez G.;	CC	1, FLAME-1 gamma, Usurpin alpha;
RT	"CLARP, a death effector domain-containing protein interacts with	CC	Name=2; Synonyms=FLIP-S, CLARE2, MRIT beta-1, CASH beta;
RT	caspase-8 and regulates apoptosis.";	CC	ISOID=O15519-2; Sequence=VSP_000828, VSP_000829;
RL	Proc. Natl. Acad. Sci. U.S.A. 94:10717-10722(1997).	CC	Name=3; Synonyms=MRIT alpha-2;
RN	[10]	CC	ISOID=O15519-3; Sequence=VSP_000824, VSP_000838;
RP	SEQUENCE FROM N.A. (ISOFORM 11).	CC	Name=4; Synonyms=I-FLICE 2;
RX	MEDLINE=21100893; PubMed=11161814; DOI=10.1006/geno.2000.6392;	CC	ISOID=O15519-4; Sequence=VSP_000825;
RA	Hadano S., Yanagisawa Y., Skaug J., Fichter K., Nasir J.,	CC	Name=5; Synonyms=I-FLICE 3;
RA	Martindale D., Koop B.F., Scherer S.W., Nicholson D.W., Rouleau G.A.,	CC	ISOID=O15519-5; Sequence=VSP_000840;
RA	Ikedo J.-E., Hayden M.R.;	CC	Name=6; Synonyms=I-FLICE 4;
RT	"Cloning and characterization of three novel genes, ALS2CR1, ALS2CR2,	CC	ISOID=O15519-6; Sequence=VSP_000826, VSP_000841;
RT	and ALS2CR3, in the juvenile amyotrophic lateral sclerosis (ALS2)	CC	Name=7; Synonyms=I-FLICE 5;
RT	critical region at chromosome 2q33-q34: candidate genes for ALS2.";	CC	ISOID=O15519-7; Sequence=VSP_000824, VSP_000827, VSP_000838;
RL	Genomics 71:200-213(2001).	CC	Name=8; Synonyms=Flame-1 alpha;
RN	[11]	CC	ISOID=O15519-8; Sequence=VSP_000830;
RP	SEQUENCE FROM N.A. (ISOFORM 1).	CC	Name=9; Synonyms=Flame-1 beta;
RC	TISSUE=Lymph;	CC	ISOID=O15519-9; Sequence=VSP_000830, VSP_000836, VSP_000837;
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;	CC	Note=May be produced at very low levels due to a premature stop
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,	CC	codon in the mRNA, leading to nonsense-mediated mRNA decay;
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,	CC	Name=10; Synonyms=Flame-1 delta;
RA	Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,	CC	ISOID=O15519-10; Sequence=VSP_000834, VSP_000835;
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,	CC	Name=11; Synonyms=Usurpin beta;
RA	Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,	CC	ISOID=O15519-11; Sequence=VSP_000838;
RA	Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,	CC	Name=12; Synonyms=Usurpin gamma;
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,	CC	ISOID=O15519-12; Sequence=VSP_000832, VSP_000833;
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,	CC	Name=13;
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,	CC	ISOID=O15519-13; Sequence=VSP_000831;
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,	CC	Name=14;
RA	Falaton D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	CC	ISOID=O15519-14; Sequence=VSP_000839;
RA	Valley J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,	CC	TISSUE SPECIFICITY: Widely expressed. Higher expression in
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,	CC	skeletal muscle, pancreas, heart, kidney, placenta, and peripheral
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,	CC	blood leukocytes. Also detected in diverse cell lines. Isoform 8
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,	CC	is predominantly expressed in testis and skeletal muscle.
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,		
RA	Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;		

CC -!- INDUCTION: Repressed by IL-2 after TCR stimulation, during
 CC progression to the S-phase of the cell cycle.

Query Match 90.8%; Score 1635; DB 1; Length 480;
 Best Local Similarity 94.1%; Pred. No. 4.3e-109;
 Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;

QY 1 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKEKSFLLDVVELEKLNIVAPDQDLDLEKCL 60

DB 97 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKEKSFLLDVVELEKLNIVAPDQDLDLEKCL 156

QY 61 KNHRIIDLTKTKIQKYSQVQAGTSTYRNVLQAAIQKSLKDPNSNNFR----- 106

DB 157 KNHRIIDLTKTKIQKYSQVQAGTSTYRNVLQAAIQKSLKDPNSNNFRHLNGRSKEQRLKEQ 216

QY 107 -----REPVKYSIQSEAFIPQSIPEERYKMKSKPLGICLIIDICIGNETELLRTFTTSLGY 162

DB 217 LGAQGPVKYSIQSEAFIPQSIPEERYKMKSKPLGICLIIDICIGNETELLRTFTTSLGY 276

QY 163 EVQKFLHLSMHGTSIQLGQFACMPHEHRDYDSFVCLVSRGSGSVYGVDTHTSGLPLHHI 222

DB 277 EVQKFLHLSMHGTSIQLGQFACMPHEHRDYDSFVCLVSRGSGSVYGVDTHTSGLPLHHI 336

QY 223 RRMFMGDSCPYLAKGPKMFPIQNYVVSQGOLEDSSLLVEDGPKMKNVFKAQKRGGLCTVH 282

DB 337 RRMFMGDSCPYLAKGPKMFPIQNYVVSQGOLEDSSLLVEDGPKMKNVFKAQKRGGLCTVH 396

QY 283 READFFWSLCTADMSLLEQSHSPSLYLQCLSQKLRQER 321

DB 397 READFFWSLCTADMSLLEQSHSPSLYLQCLSQKLRQER 435

RESULT 2

Q6QN97

ID Q6QN97 PRELIMINARY; PRT; 487 AA.

AC Q6QN97

DT 05-JUL-2004 (T-EMBLrel. 27, Created)

DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)

DE Cellular FLUICE-like inhibitory protein long form.

OS Sus scrofa (pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI_TaxID=9823;

RN [1]

RP SEQUENCE FROM N.A.

RA Goto Y., Maeda A., Matsuda F., Inoue N., Manabe N.;

RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY533021; AAS22337.1; -.

DR HSSP; P55211; IUXQ.

DR GO; GO:0030693; F:caspace activity; IEA.

DR GO; GO:0005515; F:protein binding; IEA.

DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

DR GO; GO:0042381; P:regulation of apoptosis; IEA.

DR InterPro; IPR011029; DEATH_like.

DR InterPro; IPR001875; DED.

DR InterPro; IPR001309; ICE_p20.

DR InterPro; IPR002398; Peptidase_C14.

DR Pfam; PF01335; DED; 2.

DR SMART; SM00115; CASC; 1.

DR SMART; SM00031; DED; 2.

DR PROSITE; PSS0208; CASPASE_P20; 1.

DR PROSITE; PSS0168; DED; 2.

SQ SEQUENCE 487 AA; 56000 MW; 067BE3618E9C0E7 CRC64;

Query Match 67.1%; Score 1208; DB 2; Length 487;

Best Local Similarity 69.5%; Pred. No. 2e-78;

Matches 237; Conservative 42; Mismatches 42; Indels 20; Gaps 2;

QY 1 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKEKSFLLDVVELEKLNIVAPDQDLDLEKCL 60

DB 102 MMEIGEDLDKSDVSSLIIFLMKDYMGKISKEKSFLLDVVELEKLNIVAPDQDLDLEKCL 161

QY 61 KNHRIIDLTKTKIQKYSQVQAGTSTYRNVLQAAIQKSLKDPNSNN----- 104

DB 162 KNHRIIDLTKTKIQKYSQVQAGTSTYRNVLQAAIQKSLKDPNSNNLQNGRSKEQSLIL 221

QY 105 -----FREEPVKYSIQSEAFIPQSIPEERYKMKSKPLGICLIIDICIGNETELLRTFTTSL 160

DB 222 GHPDFORDPVKTSIQESGAFLLQHVPEERYKMKSKPLGICLIIDICVGNDDTVLRTFSSL 281

QY 161 GYEVQKFLHLSMHGTSIQLGQFACMPHEHRDYDSFVCLVSRGSGSVYGVDTHTSGLPLH 220

DB 282 GYEVQKFLHLSMHGTSIQLGQFACMPHEHRDYDSFVCLVSRGSGSVYGVDTHTSGLPLD 341

QY 221 HRRFMGDSCPYLAKGPKMFPIQNYVVSQGOLEDSSLLVEDGPKMKNVFKAQKRGGLCT 280

DB 342 HRRFMGDSCPYLAKGPKMFPIQNYVVSQGOLEDSSLLVEDGPKMKNVFKAQKRGGLCT 401

QY 281 VHEADFFWSLCTADMSLLEQSHSPSLYLQCLSQKLRQER 321

DB 402 VHEADFFWSLCTADMSLLEQSHSPSLYLQCLSQKLRQER 442

RESULT 3

Q812G4

ID Q812G4 PRELIMINARY; PRT; 481 AA.

AC Q812G4

DT 01-JUN-2003 (T-EMBLrel. 24, Created)

DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)

DE CASP and FADD-like apoptosis regulator, isoform 1.

GN Name=Cflar;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=FVB/N; TISSUE=Mammary tumor;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Udell T.B., Toshlyuki S., Carninci P., Prange C.,

RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=FVB/N; TISSUE=Mammary tumor;

RA Strausberg R.; Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC029223; AAH29223.1; -.

DR HSSP; Q9C0K4; 1QTN.

DR MGD; MGI:1336166; Cflar.

DR GO; GO:0030593; F:caspace activity; IEA.

DR GO; GO:0005515; F:protein binding; IEA.

DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

DR GO; GO:0042381; P:regulation of apoptosis; IEA.

DR InterPro; IPR011029; DEATH_like.

DR InterPro; IPR001875; DED.

DR InterPro; IPR001309; ICE_p20.


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DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF01335; DED; 2.
DR SMART; SM00115; CASc; 1.
DR SMART; SM00031; DED; 2.
DR PROSITE; PS0208; CASPASE_P20; 1.
DR PROSITE; PS0168; DED; 2.
SQ SEQUENCE 481 AA; 54874 MW; 433807E2E5F5A5A05 CRC64;

Query Match          56.6%; Score 1018; DB 2; Length 481;
Best Local Similarity 62.6%; Pred. No. 8.6e-65;
Matches 211; Conservative 41; Mismatches 67; Indels 18; Gaps 5;

QY 1 MAEIGEDLDKSDVSSIFLMKQVMGRGKISKESFLDLVVELEKLNVLAPDQLDLLEKCL 60
DB LMEIGESLDQNDVSSLVFLTRDTGRGKTAKDKSFLDLVLELEKLNLIASDQLNLEKCL 161

QY 61 KNHTRDLTKTKYKQSQVGAGTSRVNLQAAIQ-SLKDPS---NNFREP----- 109
DB KNHTRIDLTKTKYKQSQGGA-RSNMNTLQASLPKLSIKYNSRLQNGRSKEPRFVEYRD 220

QY 110 -----VKKSIQSEAFLPQSIPEERYKMKSPKLGICLIIDICIGNETELLRDFTSLGYEV 164
DB SQTLLVKTISIQSEGAFLPHIREETRMQSKPLGICLIIDICIGNDKYLOETFTSLGYHI 280

QY 165 QXFLHLSMHGIIQILQGFACMPHEHDYDSFVCLVSRGGSQSYGVQDTHSGLPLHHRR 224
DB QLFLPKSHDITQIVRRYASMAHQDYDSFACVLVSLGGSQSMGDRQVHSGFSLDHVKN 340

QY 225 MFMGDSCPVLACKPKMFFTONYVSDGLEDSLLEVDGPAMKNVFEKAKGKGLCTVHRE 284
DB MFTGDTCPSLRGPKLFFQNTYESLGSLQEDSS-LEVDGFSIKNVDSKPLQPRHCTTHPE 399

QY 285 ADFFWSLCTADMSLLQSSPSLSYLQCLSKLRQER 321
DB ADFFWSLCTADVSHLEKPSSSSVYLQKLSQQLKQR 436

RESULT 4
CFLA_MOUSE
ID CFLA_MOUSE STANDARD; PRT; 484 AA.
AC 035732; 035707; 035733;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE CASP8 and FADD-like apoptosis regulator precursor (Cellular FLICE-like
DE inhibitory protein) (c-FLIP) (Caspase-eight-related protein) (Casper)
DE (Caspase-like apoptosis regulatory protein) (CLARP) (MACH-related
DE inducer of toxicity) (MRT) (Caspase homolog) (CASH) (inhibitor of
DE FLICE) (i-FLICE) (FADD-like antiapoptotic molecule 1) (Flame-1)
DE (Usurpin).
GN Name=Cflar; Synonyms=Cash;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Liver;
RX MEDLINE=97426025; PubMed=9289491; DOI=10.1074/jbc.272.32.19641;
RA Goltsev Y.V., Kovalenko A.V., Arnold E., Varfolomeev E.E.,
RA Brodianskii V.M., Wallach D.;
RT "CASH, a novel caspase homologue with death effector domains.";
RL J. Biol. Chem. 272:19641-19644 (1997).
RN [2]
SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Heart;
RX MEDLINE=97360133; PubMed=9217161; DOI=10.1038/40657;
RA Irmiler M., Thome M., Hahne M., Schneider P., Hofmann K., Steiner V.,
RA Bodmer J.-L., Schroeter M., Burns K., Mattmann C., Rimoldi D.,
RA French L.E., Tschoep J.;
RT "Inhibition of death receptor signals by cellular FLIP.";
RL Nature 388:190-195 (1997).
RN [3]

RP FUNCTION.
RX MEDLINE=20350661; PubMed=10894163; DOI=10.1016/S1074-7613(00)80214-9;
RA Yeh W.-C., Itie A., Elia A.J., Ng M., Shu H.-B., Wakeham A.,
RA Mirzios C., Suzuki N., Bonnard M., Goeddel D.V., Mak T.W.;
RT "Requirement for Casper (c-FLIP) in regulation of death receptor-
induced apoptosis and embryonic development.";
RN Immunity 12:633-642 (2000).
RL [4]

RP FUNCTION.
RX MEDLINE=20069388; PubMed=10602037;
RX DOI=10.1002/1521-4141(200001)30:1<155::AID-IMMU155>3.3.CO;2-O;
RA Wang J., Lobito A.A., Shen F., Hornung F., Winoto A., Lenardo M.J.;
RT "Inhibition of Fas-mediated apoptosis by the B cell antigen receptor
through c-FLIP.";
RL Eur. J. Immunol. 30:155-163 (2000).
CC -!- FUNCTION: Apoptosis regulator protein which may function as a
crucial link between cell survival and cell death pathways in
mammalian cells. Acts as an inhibitor of TNFRSF6 mediated
apoptosis. A proteolytic fragment (p43) is likely retained in the
death-inducing signaling complex (DISC) thereby blocking further
recruitment and processing of caspase-8 at the complex. Full
length and shorter isoforms have been shown either to induce
apoptosis or to reduce TNFRSF-triggered apoptosis. Lacks enzymatic
(caspase) activity (By similarity).
CC -!- SUBUNIT: TNFRSF6 stimulation triggers recruitment to the death-
inducing signaling complex (DISC) formed by TNFRSF6, FADD and
caspase-8. A proteolytic fragment (p43) stays associated with the
DISC (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Name=1; Synonyms=FLIP-L, CASH alpha;
IsoId=O35732-1; Sequence=Displayed;
Name=2; Synonyms=FLIP-S, CASH beta;
IsoId=O35732-2; Sequence=VSP_000842, VSP_000843;
CC -!- TISSUE SPECIFICITY: Highly expressed in heart.
CC -!- DEVELOPMENTAL STAGE: At embryonic days E9.5 and E10.5 highest
expression in developing heart.
CC -!- INDUCTION: Isoform 1 but not isoform 2 is activated by BCR cross-
linking in primary B-cells.
CC -!- DOMAIN: The caspase domain lacks the active sites residues
involved in catalysis.
CC -!- PTM: Proteolytically processed; probably by caspase-8. Processing
likely occurs at the DISC, generates subunit p43 and p12 (By
similarity).
CC -!- SIMILARITY: Belongs to the peptidase C14 family.
CC -!- SIMILARITY: Contains 2 death effector (DED) domains.
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EMBL; Y14041; CAA74368.1; -.
DR EMBL; Y14042; CAA74369.1; -.
DR EMBL; U97076; AAC53281.1; -.
DR HSSP; Q9C0K4; IQTN.
DR MEROPS; C14.974; -.
DR MGD; MGI:1336166; Cflar.
DR InterPro; IPR011029; DEATH_like.
DR InterPro; IPR001875; DED.
DR InterPro; IPR001309; ICE_p20.
DR Pfam; PF01335; DED; 2.
DR PROSITE; PS0208; Peptidase C14; 1.
DR PROSITE; PS0168; CASPASE_P20; 1.
KW Alternative splicing; Apoptosis; Repeat.
CHAIN 1 380 CASP8 and FADD-like apoptosis regulator
subunit p43 (By similarity).
CHAIN 381 484 CASP8 and FADD-like apoptosis regulator
subunit p12 (By similarity).
FT
```



```
Q8UVG5
ID Q8UVG5 PRELIMINARY; PRT; 418 AA.
AC Q8UVG5;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Clap1.
GN Name=cf1ar;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98021435; PubMed=9380701; DOI=10.1073/pnas.94.20.10717;
RA Inohara N., Koseki T., Hu Y., Chen S., Nunez G.;
RT "CLARP, a death effector domain-containing protein interacts with
RT caspase-8 and regulates apoptosis."
RL Proc. Natl. Acad. Sci. U.S.A. 94:10717-10722(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20373792; PubMed=10917738;
RA Inohara N., Nunez G.;
RT "Genes with homology to mammalian apoptosis regulators identified in
RT zebrafish."
RL Cell Death Differ. 7:509-510(2000).
RN [3]
RP SEQUENCE FROM N.A.
RA Inohara N., Nunez G.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF448261; AAL41007.1; -.
DR HSSP; P5210; 1140.
DR ZFIN; ZDB-GENE-030826-3; cf1ar.
DR GO; GO:003693; F:caspase activity; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR GO; GO:0042981; P:regulation of apoptosis; IEA.
DR Pfam; PF01335; DED; 2.
DR SMART; SM00115; CASG; 1.
DR SMART; SM00031; DED; 2.
DR PROSITE; P50208; CASPASE_P20; 1.
DR PROSITE; P50168; DED; 2.
SQ SEQUENCE 418 AA; 47618 MW; C2ECB3AE571E0237 CRC64;

Query Match 26.2%; Score 471; DB 2; Length 418;
Best Local Similarity 34.2%; Pred. No. 1.4e-25;
Matches 118; Conservative 59; Mismatches 102; Indels 66; Gaps 11;

QY 1 MAEIGEDLDKSDVSSLIPLMKDYMGRGKISKEKSFLLDVVELEKLNVLAPDQDLLEKCL 60
||:|||||:|||||: : : : : |||||: : : |||||: : : |||||
106 MADVSENLDKEDLQSLIFLLSSILPKERSTRATSFLLDVVELEKLNVEKCLDFLEKCL 165

QY 61 KNHRIIDLTKTKQYKQSVQAGTSYRNVLQAAIQKSLKDPNNFEEPVKKSIOESEAF 120
|||||:|||||:|||||: : : : : |||||: : : |||||: : : |||||
166 KNIRNDLVKKIQAYRNQGNPCAPNTFKETPMQC-----QPFKQVRQSCF 215

QY 121 -----LPOSIDE-----ERYKMSKPLGICLIIDICIGNETELLARDFTSLGY-- 162
||:|||||:|||||: : : : : |||||: : : |||||: : : |||||
216 NHEFNKLLKLSVPTGTHYQQAITEEYQMPNQEGLCVIIDCVGYDGEMLKHTFECLGFKV 275

QY 163 -----EVQKFLH-LSMHGISQITLQGFACMPHEHRDVSFVCLVIRGGSGSVVGVQ 212
||:|||||:|||||: : : : : |||||: : : |||||: : : |||||
276 VFHSLILGLKETQKLEDLNLRILQVRVRC-----FVCLISRGTNTHLLATDS 323

QY 213 THSGPLPHHIRMFMGDSCPYLAKPKMFFIQNYVVSQDGL---EDSSLLEVDGPKMKV 269
||:|||||:|||||: : : : : |||||: : : |||||: : : |||||
324 NRLGINLKDQLFNATKC-----PKIFFTQLYRITAEAPVMPMDLEYLETDA PASR-- 375

QY 270 EFKAQRGLCTVHREADFWSLCTADMSLLEQSHSPSLYLQCLS 314
||:|||||:|||||: : : : : |||||: : : |||||: : : |||||
376 ----QCSNTGTVMPMPADVLWSVCTAEVKLEES-GHQSVILNALN 415
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RESULT 7
Q6QN98 PRELIMINARY; PRT; 219 AA.
ID Q6QN98
AC Q6QN98;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cellular FLIC-like inhibitory protein short form.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Goto Y., Maeda A., Matsuda F., Inoue N., Manabe N.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY533020; AAS22336.1; -.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0042981; P:regulation of apoptosis; IEA.
DR InterPro; IPR011029; DEATH_like.
DR InterPro; IPR001875; DED.
DR Pfam; PF01335; DED; 2.
DR SMART; SM00031; DED; 2.
DR PROSITE; P50168; DED; 2.
SQ SEQUENCE 219 AA; 25303 MW; 840DC7135D88AAC8 CRC64;

Query Match 22.4%; Score 403.5; DB 2; Length 219;
Best Local Similarity 75.7%; Pred. No. 4.2e-21;
Matches 81; Conservative 12; Mismatches 13; Indels 1; Gaps 1;

QY 1 MAEIGEDLDKSDVSSLIPLMKDYMGRGKISKEKSFLLDVVELEKLNVLAPDQDLLEKCL 60
|||||:|||||:|||||: : : : : |||||: : : |||||: : : |||||
102 MMEIGELDKSDVSSLIPLMRDHISRSKWAKDKSFLDVVIELEKLNVLAPDHLDLLEKCL 161

QY 61 KNHRIIDLTKTKQYKQSVQAGTSYRNVLQAAIQK-SLKDPNNFR 106
|||||:|||||:|||||: : : : : |||||: : : |||||: : : |||||
162 RNHRIIDLTKTKQYKQAGTAETVYVNALQASLPNLKIDPSYNLR 208

RESULT 8
Q99MZ5 PRELIMINARY; PRT; 218 AA.
ID Q99MZ5
AC Q99MZ5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE FLIP short form.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=22131045; PubMed=12135878;
RA Xiao C.W., Asselin E., Tsang B.K.;
RT "Nuclear factor kappaB-mediated induction of Flice-like inhibitory
RT protein prevents tumor necrosis factor alpha-induced apoptosis in rat
RT granulosa cells."
RL Biol. Reprod. 67:436-441(2002).
DR EMBL; AF244366; AAK28358.1; -.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0042981; P:regulation of apoptosis; IEA.
DR InterPro; IPR011029; DEATH_like.
DR InterPro; IPR001875; DED.
DR Pfam; PF01335; DED; 2.
DR SMART; SM00031; DED; 2.
DR PROSITE; P50168; DED; 2.
SQ SEQUENCE 218 AA; 24718 MW; 9DA9EBAF3441967B CRC64;

Query Match 19.2%; Score 345; DB 2; Length 218;
Best Local Similarity 67.3%; Pred. No. 6.7e-17;
```


RA Fernandes-Alnemri T., Croce C.M., Litwack G., Tomaselli K.J.,
RA Armstrong R.C., Alnemri E.S.;
RT "FLAME-1, a novel FADD-like anti-apoptotic molecule that regulates
RT Fas/TNFR1-induced apoptosis.";
RL J. Biol. Chem. 272:18542-18545 (1997).
RN [16]
RN SEQUENCE FROM N.A.
RP MEDLINE=21100893; PubMed=11161814; DOI=10.1006/geno.2000.6392;
RX Hadano S., Yanagisawa Y., Skaug J., Fichter K., Nasir J.,
RA Martindale D., Koop B.F., Scherer S.W., Nicholson D.W., Rouleau G.A.,
RA Ikeda J.-E., Hayden M.R.;
RT "Cloning and characterization of three novel genes, ALS2CR1, ALS2CR2,
RT and ALS2CR3, in the juvenile amyotrophic lateral sclerosis (ALS2)
RT critical region at chromosome 2q33-q34: candidate genes for ALS2";
RL Genomics 71:200-213 (2001).
RN [7]
RN SEQUENCE FROM N.A. (ISOFORM 7), AND FUNCTION OF ISOFORM 7.
RP TISSUE=Leukocyte;
RX MEDLINE=22005982; PubMed=12010809; DOI=10.1182/blood.V99.11.4070;
RA Himeji D., Horiuchi T., Tsukamoto H., Hayashi K., Watanabe T.,
RA Harada M.;
RT "Characterization of caspase-8L: a novel isoform of caspase-8 that
RT behaves as an inhibitor of the caspase cascade.";
RL Blood 99:4070-4078 (2002).
RN [8]
RN SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 9), AND INTERACTION OF ISOFORM 9
RP WITH BCAP31 AT THE ENDOPLASMIC RETICULUM.
RX MEDLINE=21927603; PubMed=11917123; DOI=10.1073/pnas.072088099;
RA Breckenridge D.G., Nguyen M., Kuppig S., Reth M., Shore G.C.;
RT "The procaspase-8 isoform, procaspase-8L, recruited to the BAP31
RT complex at the endoplasmic reticulum";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4331-4336 (2002).
RN [9]
RN SEQUENCE FROM N.A. (ISOFORM 7).
RP TISSUE=Leukocyte;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klusner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinaki M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [10]
RN PARTIAL SEQUENCE, AND PROCESSING.
RX MEDLINE=97121412; PubMed=8962078; DOI=10.1073/pnas.93.25.14486;
RA Sriniwasula S.M., Ahmad M., Fernandes-Alnemri T., Litwack G.,
RA Alnemri E.S.;
RT "Molecular ordering of the Fas-apoptotic pathway: the Fas/APO-1
RT protease Mch5 is a CrmA-inhibitable protease that activates multiple
RT Ced-3/ICE-like cysteine proteases";
RL Proc. Natl. Acad. Sci. U.S.A. 93:14486-14491 (1996).
RN [11]
RN FUNCTION.
RX MEDLINE=97160607; PubMed=9006941; DOI=10.1074/jbc.272.5.2952;
RA Muzio M., Salvesen G.S., Dixit V.M.;
RT "FLICE induced apoptosis in a cell-free system. Cleavage of caspase
RT zymogens.";
RL J. Biol. Chem. 272:2952-2956 (1997).
RN [12]
RN PROCESSING.
RX MEDLINE=97327557; PubMed=9184224; DOI=10.1093/emboj/16.10.2794;
RA Medina J.P., Scaffidi C., Kischkel F.C., Shevchenko A., Mann M.,
RA Kramer P.H., Peter M.E.;
RT "FLICE is activated by association with the CD95 death-inducing
RT signaling complex (DISC).";
RL EMBO J. 16:2794-2804 (1997).
RN [13]
RN CHARACTERIZATION OF ISOFORM 7.
RP MEDLINE=20318377; PubMed=10860845; DOI=10.1006/bbrc.2000.2841;
RA Horiuchi T., Himeji D., Tsukamoto H., Harashima S., Hashimura C.,
RA Hayashi K.;
RT "Dominant expression of a novel splice variant of caspase-8 in human
RT peripheral blood lymphocytes.";
RL Biochem. Biophys. Res. Commun. 272:877-881 (2000).
RN [14]
RN INTERACTIONS WITH BCL2; BCL2L1 AND BCAP31.
RX MEDLINE=97477382; PubMed=9334338; DOI=10.1083/jcb.139.2.327;
RA Ng F.W.H., Nguyen M., Kwan T., Branton P.E., Nicholson D.W.,
RA Cromlish J.A., Shore G.C.;
RT "p28 Bap31, a Bcl-2/Bcl-xL- and procaspase-8-associated protein in the
RT endoplasmic reticulum";
RL J. Cell Biol. 139:327-338 (1997).
RN [15]
RN INTERACTION WITH PEA15.
RP MEDLINE=99369240; PubMed=1042631; DOI=10.1038/sj.onc.1202831;
RA Condorelli G., Vigliotta G., Cafieri A., Trencia A., Andalo P.,
RA Oriente F., Mele C., Caruso M., Fornisano P., Beguinot F.;
RT "PBD/PEA-15: an anti-apoptotic molecule that regulates Fas/TNFR1-
RT induced apoptosis.";
RL Oncogene 18:4409-4415 (1999).
RN [16]
RN SPLICE ISOFORM(S) THAT ARE POTENTIAL NMD TARGET(S).
RX PubMed=14759258; DOI=10.1186/gb-2004-5-2-r8;
RA Hillman R.T., Green R.E., Bremner S.E.;
RT "An unappreciated role for RNA surveillance.";
RL Genome Biol. 5:RESEARCH008.1-RESEARCH008.16 (2004).
RN [17]
RN X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
RX MEDLINE=99451259; PubMed=10508784; DOI=10.1016/S0969-2126(99)80179-8;
RA Blanchard H., Kodandapani L., Mittl P.R.E., Di Marco S., Krebs J.F.,
RA Wu J.C., Tomaselli K.J., Gruetter M.G.;
RT "The three-dimensional structure of caspase-8: an initiator enzyme in
RT apoptosis";
RL Structure 7:1125-1133 (1999).
RN [18]
RN VARIANT CASP8D TRP-248.
RX MEDLINE=22239940; PubMed=12353035; DOI=10.1038/nature01063;
RA Chun H.-J., Zheng L., Ahmad M., Wang J., Speirs C.K., Siegel R.M.,
RA Dale J.K., Puck J., Davis J., Hall C.G., Skoda-Smith S.,
RA Atkinson T.P., Straus S.E., Lenardo M.J.;
RT "Pleiotropic defects in lymphocyte activation caused by caspase-8
RT mutations lead to human immunodeficiency.";
RL Nature 419:395-399 (2002).
RN CC -!- FUNCTION: Most upstream protease of the activation cascade of
CC caspases responsible for the TNFRSF6/Fas mediated and TNFRSF1A
CC induced cell death. Binding to the adapter molecule FADD recruits
CC it to either receptor. The resulting aggregate called death-
CC inducing signaling complex (DISC) performs CASP8 proteolytic
CC activation. The active dimeric enzyme is then liberated from the
CC DISC and free to activate downstream apoptotic proteases.
CC Proteolytic fragments of the N-terminal propeptide (termed CAP3,
CC CAP5 and CAP6) are likely retained in the DISC. Cleaves and
CC activates CASP3, CASP4, CASP6, CASP7, CASP9 and CASP10. May
CC participate in the GZMB apoptotic pathways. Cleaves ADPRT.
CC Hydrolyzes the small-molecule substrate, Ac-Asp-Glu-Val-Asp-|-AMC.
CC Likely target for the cowpox virus CMA death inhibitory protein.
CC Isoforms 5, 6, 7 and 8 lack the catalytic site and may interfere
CC with the pro-apoptotic activity of the complex.
CC -!- SUBUNIT: Heterodimer of a 18 kDa (p18) and a 10 kDa (p10) subunit.
CC Interacts with FADD, CFLAR and PEA15. Isoform 9 interacts at the
CC endoplasmic reticulum with a complex containing BCAP31, BAP29,
CC BCL2 and/or BCL2L1.

CC -i- SUBCELLULAR LOCATION: Cytoplasmic.

Query Match 17.48; Score 313; DB 1; Length 479;
Best Local Similarity 26.84; Pred. No. 3.5e-14;
Matches 95; Conservative 75; Mismatches 117; Indels 68; Gaps 14;

QY 3 EIGEDLDKSDVSSLI FLMDYMGKSKSFLDLVVELEKLNVLAPDQDLLEKCKN 62
DB 107 QISEEVSRLSPFKFLQGEISKLDLDDNLLDIFIEKRVILGEGKDLKRVCAQ 166
QY 63 IHRIDLTKIYKQKQ-----SVQAGTSYRNVLQAAIQKSLKDPNPNFREPVKSIQ 115
DB 167 INKSLIK-KIEDYELNLLGEG-----EMLVTEGQSSSTGAPDSRAIWLASSVAP 214
QY 123 QSIPE-----ERYKMKSKPLGICLI I-----DCIGN--ETELLR 154
DB 215 DSLGNCDCQSSQLEVYKWTSRPRGVCILINNHNFAKAREAVPELRMRKDRNGTHVDADAR 274
QY 155 DTFTSLGYEVOKFLHLSMHGISOILQGFACMPHRRDYDFVCLVSRGGSQSVGVDOOTH 214
DB 275 KVFESNLHFTVAEYKDCITABEIRNVNRYCM-DHNNKDCFCVCCILSHGKKDIYGVGDQE 333
QY 215 SGPLPHHIRMFMGDCSPYLAGPKMFFIQNYVVSQGLSDSLLEV-D-GPAMKNVFEKA 273
DB 334 --VPIQLTTSFTGQNCQSLAGPKVFFVQ--ACQGDAYQKGVITFDSGEQDYSLETDA 389
QY 274 QKRGCLTVHREADFFWSLCTADMSLLEQSHSPSLYLQCLSKQL 317
DB 390 RFQLDC-IPSEADFLGTMITLQDYVSVSRPSQGTWYIQLCOHL 432

RESULT 12
ICE8_MOUSE
ID ICE8_MOUSE STANDARD; PRT; 480 AA.
AC O89110; O35669;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Caspase-8 precursor (BC 3.4.22.-) (CASP-8).
GN Name=Casp8;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN=129/SvJ;
RX MEDLINE=98316661; PubMed=9654089;
RA Sakamaki K., Teukumo S.-I., Yonehara S.;
RT "Molecular cloning and characterization of mouse caspase-8.";
RL Eur. J. Biochem. 253:399-405(1998).
RN [2]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RX MEDLINE=99057979; PubMed=9837723; DOI=10.1006/jmbi.1998.2226;
RA Van de Craen M., Van Loo G., Declercq W., Schotte P.,
RA van den Brande I., Mandruzzato S., van der Bruggen P., Fiers W.,
RA Vandenabeele P.;
RT "Molecular cloning and identification of murine caspase-8.";
RL J. Mol. Biol. 284:1017-1026(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Colon, and Mammary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Cantancini P., Prange C.,
RA Baha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

QY 3 EIGEDLDKSDVSSLI FLMDYMGKSKSFLDLVVELEKLNVLAPDQDLLEKCKN 62
DB 107 QISEEVSRLSPFKFLQGEISKLDLDDNLLDIFIEKRVILGEGKDLKRVCAQ 166
QY 63 IHRIDLTKIYKQKQ-----SVQAGTSYRNVLQAAIQKSLKDPNPNFREPVKSIQ 115
DB 167 INKSLIK-KIEDYELNLLGEG-----EMLVTEGQSSSTGAPDSRAIWLASSVAP 214
QY 116 ESEAFUPOSPEERYKMKSKPLGICLIIDCIG-----NETEL-----LR 154
DB 216 DSES--QTL-DKYQMKSPRGVCILINNHNFAKAREKVPKLHSIRDRNGTHLDAGALT 271
QY 155 DTFTSLGYEVOKFLHLSMHGISOILQGFACMPHRRDYDFVCLVSRGGSQSVGVDOOTH 214
DB 272 TTEELHFEIKPHDDCTVEQIYELIKIYQLM-DHSNWDCCFICILSHGDKGIYGTGQE 330
QY 215 SGPLPHHIRMFMGDCSPYLAGPKMFFIQ-----NY---VVSQGLSDSLLEV-D-GP 264
DB 331 A--PIVELTSQFTGLKCPSLAGPKVFFIQAQCGDNVQKGI PVETDSEQPYLEMDLSSP 388
QY 265 AMKNVFEKAKRGCLTVHREADFFWSLCTADMSLLEQSHSPSLYLQCLSKQLRQ 319
DB 389 QTRYIP-----DEADFLGTMATVNCVSRNPAETGWTYIQLCOQLSRL 431

RESULT 11
Q90WU1 PRELIMINARY; PRT; 482 AA.
AC Q90WU1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Caspase 8.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Barton S., Bridgham J.T., Johnson A.L.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
CC -i- SIMILARITY: Belongs to the peptidase C14 family.
DR EMBL; AY057939; AAL23700.1; -;
DR HSSP; Q9COK4; IODU.
DR MEROPS; C14.009; -;
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0008234; F:cysteine-type peptidase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR GO; GO:0042981; P:regulation of apoptosis; IEA.
DR PFAM; PF01335; DED; 2.
DR PRINTS; PR00376; ILIBCNZYME.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; UNKNOWN_1.
DR PROSITE; PS02027; CASPASE_P10; 1.
DR PROSITE; PS02028; CASPASE_P20; 1.
DR PROSITE; PS0168; DED; 2.
KW Hydrolase; Protease; Thiol protease; Zymogen.
SQ SEQUENCE 482 AA; 54645 MW; 8E3936B6EE090BEF CRC64;

Query Match 16.84; Score 302.5; DB 2; Length 482;
Best Local Similarity 25.98; Pred. No. 2e-13;
Matches 89; Conservative 67; Mismatches 141; Indels 47; Gaps 10;


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Query Match 15.4%; Score 277; DB 2; Length 78;
Best Local Similarity 73.1%; Pred. No. 1.4e-12;
Matches 57; Conservative 2; Mismatches 1; Indels 18; Gaps 1;

QY 86 YRNLVQAQKSLKDPNNPFR-----EPPVKGIQSEAFLPQSIPE 127
Db 1 YKVLQAQKSLKDPNNPFRHLNGRSKEORLKEQLGTQEPVKYIQSEAFLPQSIPE 60

QY 128 ERYKMSKPLGICLIIDC 145
Db 61 ERYKMSKPLGICLIIDC 78

RESULT 14
ID Q6PAD9 PRELIMINARY; PRT; 512 AA.
AC Q6PAD9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE MGC68465 protein.
GN Name=MGC68465;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative."
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (Oct-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the peptidase C14 family.
DR EMBL; BC060356; AAH60356.1; -.
DR HSP; P55210; 1K86.
DR GO; GO:0030693; F:casein activity; IEA.
DR GO; GO:0008234; F:cysteine-type peptidase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0005515; F:protein binding; IEA.

DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR GO; GO:0042981; P:regulation of apoptosis; IEA.
DR InterPro; IPR011029; DEATH_like.
DR InterPro; IPR001875; DED.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF01335; DED; 2.
DR PRINTS; PR00376; IL1BCENZYM.
DR SMART; SM00115; CASC; 1.
DR SMART; SM00031; DED; 2.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS0207; CASPASE_P10; 1.
DR PROSITE; PS0208; CASPASE_P20; 1.
DR PROSITE; PS0168; DED; 2.
KW Hydrolase; Protease; Thiol protease; Zymogen.
SQ SEQUENCE 512 AA; 58799 MW; FE91F00AD8C0EFBB CRC64;

Query Match 15.0%; Score 270; DB 2; Length 512;
Best Local Similarity 27.5%; Pred. No. 4.7e-11;
Matches 100; Conservative 55; Mismatches 142; Indels 66; Gaps 14;

QY 3 EIGEDLDKSDVSSLIFLMKDYMGKGIKSKSPFLDLVLEKLNVLVAPDQLLEKLN 62
Db 104 ELSNVTGDDKRIILFLP---FQKHKNKTFDLVLCLEKENSITDNVGLLEDFK 160
QY 63 IHRIDLTKIKYKQ---SVQ-GAGTSYRNL---AAIQKSLKDPN----- 103
Db 161 VSP-DLLKTIKYKERENNLQSPAPPEYEHLELNPPLSIQVSSKNNSWNEETDLIEH 219
QY 104 -NPREPVK-----SIQSEAFLPQ-SIPERYKMSKPLGICLIID-----C 145
Db 220 GTIHEAEKEDDKSGNIDQLDLRLNPITPOASLMELYDMNRKRGYCLIIDNSIFA 279
QY 146 IGNETE-----LLRDTFTSLGYEQKFLHLSMHGISQILGQFACMPHERDYDSFVCVL 198
Db 280 KGKRGSKDAGALRDVFNGLDVEIVENLGSEIRDKFK-KDHSERDCVCCI 338
QY 199 VGRGSGSYGVVDQTHSGPLHHRMFMGDSCPYLAGPKMFFIQ-----NYVVDGQLE 254
Db 339 LTHGSGTVLGSDEE--VSIREIMSYFTPTSCLSLALKPKLFFIQACQGRYTHPSKVE 396
QY 255 DSSLLEVDGPMKNVFEKQKRGCLCTVHEADFWSLCTADMSLLSQSHSPSLYLQCLS 314
Db 397 ADATVPVE-----HKYIVNVKPEADFLGMSTVDGYFAFRHRTSGSWYIQALC 445
QY 315 QKL 317
Db 446 KNL 448

RESULT 15
QY1B62 PRELIMINARY; PRT; 520 AA.
AC QY1B62;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Caspase-10 (Xcaspase-10 protein).
GN Name=xCaspase-10;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20209426; PubMed=10744739; DOI=10.1074/jbc.275.14.10484;
RA Nakajima K., Takahashi A., Yaoita Y.;
RT "Structure, expression and function of the Xenopus laevis caspase
RT family."
RL J. Biol. Chem. 275:10484-10491(2000).
```

[2]
RN
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=223889257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.C., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grigwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski W.I., Skalska U., Smalls D.B., Schnerch A., Schein J.E.,
RA Jones S.-J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3].

SEQUENCE FROM N.A.
RN
RP TISSUE=Embryo;
RC RC
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [4].

SEQUENCE FROM N.A.
RN
RP TISSUE=Embryo;
RC RC
RX Klein S., Strausberg R.;
RL Submitted (APR-2004) to the ENBL/GenBank/DBBJ databases.
CC -I- SIMILARITY: Belongs to the peptidase C14 family.
DR ENBL; AB038173; BAA94751.1; -.
DR ENBL; BC068638; AAH68638.1; -.
DR HSSP; QPCOK4; IQTN.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0008234; F:cysteine-type peptidase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR GO; GO:0042981; P:regulation of apoptosis; IEA.
DR InterPro; IPR011029; DEATH_like.
DR InterPro; IPR001875; DED.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF01335; DED; 2.
DR PRINTS; PR00376; IL1BCENZYM.
DR SMART; SM00115; CASc; 1.
DR SMART; SM00031; DED; 2.
DR PROSITE; PS01122; CASPAGE_CYS; 1.
DR PROSITE; PS01121; CASPAGE_HIS; 1.
DR PROSITE; PS0207; CASPAGE_P10; 1.
DR PROSITE; PS0208; CASPAGE_P20; 1.
DR PROSITE; PS0168; DED; 2.
KW Hydrolase; Protease; Thiol protease; Zymogen.
SQ SEQUENCE 520 AA; 59626 MW; 33164A5A09CA6615 CRC64;

Query Match 14.8%; Score 267; DB 2; Length 520;
Best Local Similarity 26.3%; Pred. No. 7.9e-11;
Matches 98; Conservative 54; Mismatches 143; Indels 78; Gaps 13

QY 3 ETGEDLDKSDVSLFLPKMDYMGKTSIKESFTDLVVVELEKLNVAPDGLLEKLN 62
Db 104 ELSENVTGDEKRIFLPLHK---KKKENKTFTVLQLEKNAITDNVKLEVFPRK 160

```

Qy 63 IHRIDLTKYIKYKO-----SVQAGCTSYRNVL---QAAIQKSLKDPSSNPRE 10
Db 161 VSP-DLLKXIIIEKYERGDKLHPEIGLMQPSAPPDYEHHELINPHLSIQVSSKK--NESMD 217
Qy 108 EPVKKSIOSEBAFL-----PO-SIPEERYKMKSKPLGI 139
Db 218 EGIESLIEHNGTILGEAEKEDDESGNIDHQLSDLRLNSEVTPQASIQOMELYHNMHKRGV 277
Qy 140 CLIID-----CIGNETE-----LLRDTFTSLGYEVOKFLHLSMHGSIQILGOFACMPEH 188
Db 278 CLIIDNSIFMGKREGSKDAGALSDVFSWGLGLEIVEIKNLGTEQIRGCLKRFK-SKH 336
Qy 189 RYDSEFVCLVSRGGSQSVYGDQTHSGLPLIHIRRMFMGSDSPYLAGKQPMFIQN--- 245
Db 337 SERDCFVCCILTHGSEGTVMGSDDKK--VSIREVMSYFTATSCITSLTLKPLFFIQACQG 394
Qy 246 -VVSDGQLEDSSLLEVDGPMKKNVEFKAKRGICLTVHREADFFWSLCTADMSLLSQSHS 304
Db 395 IYTHPSKVPEDASVPVE-----HKYIIVNVFKPADFLGLNSTVDGYAAYRHKK 443
Qy 305 SPSLYLQCLLSQKL 317
Db 444 YGSWYIQALCKNL 456

Search completed: June 20, 2005, 13:05:20
Job time : 177 secs

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Search completed: June 20, 2005, 13:05:20
Job time : 177 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2005, 12:43:37 ; Search time 166 Seconds
(without alignments)
810.799 Million cell updates/sec

Title: US-10-713-208-6
Perfect score: 1800
Sequence: 1.MAEGEDLDKSDVSSLIPLM.....ITESKDMHPSLGCILLDVL 348

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1800	100.0	348	2	AAW69230 I-FLICE-2
2	1800	100.0	348	7	ADA10619 Human inh
3	1800	100.0	348	7	ADF76399 Novel hum
4	1800	100.0	348	8	ADJ96514 Human I-F
5	1800	100.0	348	8	ADJ96514 Human inh
6	1774	98.6	366	2	AAW05788 Human MAC
7	1774	98.6	422	3	AAW67419 Usurpin-b
8	1774	98.6	462	8	ADRI4101 Human NF-
9	1635	90.8	384	2	AAW05791 MRIT alph
10	1635	90.8	480	2	AAW58578 Human FIN
11	1635	90.8	480	2	AAW69715 Human Cas
12	1635	90.8	480	2	AAW69229 I-FLICE-1
13	1635	90.8	480	2	AAW76631 Human CFL
14	1635	90.8	480	2	AAW05787 Human MAC
15	1635	90.8	480	2	AAW57454 Human FLI
16	1635	90.8	480	3	AAW57606 Human apo
17	1635	90.8	480	3	AAW67418 Usurpin-a
18	1635	90.8	480	3	AAW03960 FLICE-lik
19	1635	90.8	480	5	ABW09294 Human FLI
20	1635	90.8	480	7	ADA10615 Human inh
21	1635	90.8	480	8	ADJ96510 Human I-F
22	1635	90.8	480	8	ADRI1312 Human inh
23	1635	90.8	491	3	AAW03964 FLIP with
24	1630	90.6	391	4	AAW09601 Human gen
25	1630	90.6	391	4	AAU21591 Novel hum

26	1630	90.6	391	5	ABG78973 Human apo
27	1630	90.6	391	7	ADC46232 Human neo
28	1630	90.6	391	7	AAE39801 Human gen
29	1630	90.6	480	2	AAW78903 Human G1
30	1630	90.6	480	7	ADN95807 Human BEC
31	1630	90.6	480	8	ADP54877 Human PRO
32	1618	89.9	479	2	AAW76625 Human FLI
33	1579	87.7	480	3	AAW59414 Human CLA
34	1579	87.7	480	7	ADJ68469 Human FLI
35	1554.5	86.4	445	5	AAE26086 Human FLA
36	1554.5	86.4	445	5	AAE26086 Human FLA
37	1229	68.3	302	2	AAW05792 MRIT-ND1
38	1128	62.7	264	2	AAW05790 Human ant
39	1018	56.6	481	2	AAW76632 Mouse CFL
40	1018	56.6	481	3	AAW03958 FLICE-lik
41	1018	56.6	481	5	ABW09295 Mouse FLI
42	1018	56.6	483	2	AAW76626 Murine FL
43	1006.5	55.9	484	5	ABW09292 Mouse FLI
44	1006.5	55.9	484	6	ABW99383 Amino aci
45	978	54.3	230	2	AAW05793 MRIT-Bam

ALIGNMENTS

RESULT 1

AAW69230
ID AAW69230 standard; protein; 348 AA.

XX
AC AAW69230;

XX
DT 18-FEB-1999 (first entry)

XX
DE I-FLICE-2.protein.

XX
KW I-FLICE-2; FADD like ICE protein; inhibitor; TNFR-1; Alzheimer's disease;
CD-95 induced apoptosis; Parkinson's disease; rheumatoid arthritis;
CNS inflammation; osteoporosis; ischaemia; polycystic kidney disease;
multiple sclerosis; head injury; cancer; autoimmune disorder; therapy;
viral infection; graft versus host disease; graft rejection.

XX
OS Homo sapiens.

XX
PN WO9831801-A1.

XX
PD 23-JUL-1998.

XX
PF 21-JAN-1998; 98WO-US000969.

XX
PR 21-JAN-1997; 97US-0034205P.

XX
PR 05-AUG-1997; 97US-0054800P.

XX
PA (HUMA-) HUMAN GENOME SCI INC.

XX
PA (UNMI) UNIV MICHIGAN.

XX
PI Ni J, Rosen CA, Dixit VM, Gentz RL, Kenny JJ;

XX
WPI; 1998-414100/35.

XX
N-PSDB; AAW44807.

XX
PT New inhibitory polypeptides of FLICE - used to develop products for
treating e.g. Alzheimer's disease, sepsis, stroke, osteoporosis, cancers,
autoimmune disorders, viral infection or graft rejection.

XX
PS Claim 9; Fig 4; 118pp; English.

XX
CC This sequence is an inhibitor of Fas-ligand associated with death
domain (FADD) like ICE (I-FLICE) protein, designated I-FLICE-2. The
proteins can inhibit both TNFR-1 and CD-95 induced apoptosis. These are
the first examples of a naturally occurring catalytically inactive
caspase that can act as a dominant negative inhibitor of apoptosis. The
polypeptides and agonists can be used for treating e.g. Alzheimer's
disease, Parkinson's disease, rheumatoid arthritis, septic shock, sepsis,

CC stroke, CNS inflammation, osteoporosis, ischaemia, reperfusion injury,
 CC cell death associated with cardiovascular disease, polycystic kidney
 CC disease, apoptosis of endothelial cells in cardiovascular disease,
 CC degenerative liver disease, multiple sclerosis (MS) and head injury
 CC damage. Antagonists of the polypeptides can be used for treating cancers
 CC (e.g. follicular lymphomas, carcinomas with p53 mutations, hormone-
 CC dependent tumours, and cancers of the breast, ovary, prostate, bone,
 CC liver, lung, pancreas, and spleen), autoimmune disorders (e.g. systemic
 CC lupus erythematosus, immune-related glomerulonephritis, rheumatoid
 CC arthritis), and viral infections (e.g. herpes viruses, pox viruses and
 CC adenoviruses), graft versus host disease, acute disease, acute graft
 CC rejection, and chronic graft rejection. The products can also be used for
 CC detection, diagnosis and drug screening
 XX
 SQ Sequence 348 AA;

Query Match 100.0%; Score 1800; DB 2; Length 348;
 Best Local Similarity 100.0%; Pred. No. 1.7e-171;
 Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEIGEDLDKSDVSSLIFLMKDYMGRGKISKEKSFLLDVVELEKLNLVAPDQDLLEKCL 60
 DB 1 MAEIGEDLDKSDVSSLIFLMKDYMGRGKISKEKSFLLDVVELEKLNLVAPDQDLLEKCL 60
 QY 61 KNHRIIDLTKIKYKQSVQAGTGYRNVLAQAIQKSLKDPNNFPREPVKKSIOSEAF 120
 DB 61 KNHRIIDLTKIKYKQSVQAGTGYRNVLAQAIQKSLKDPNNFPREPVKKSIOSEAF 120
 QY 121 LPQSIPEERYKMKSPGLGICLIIDICIGNETELLRTFTSLGYEVQKFLHLSMHGISOILG 180
 DB 121 LPQSIPEERYKMKSPGLGICLIIDICIGNETELLRTFTSLGYEVQKFLHLSMHGISOILG 180
 QY 181 QFACMPEDRDYDFVCVLVSRGSGSVGVGDQTHSGPLPHHIRMFMGDSFCPLACKPKM 240
 DB 181 QFACMPEDRDYDFVCVLVSRGSGSVGVGDQTHSGPLPHHIRMFMGDSFCPLACKPKM 240
 QY 241 FFIQNVVSDGQLEDSSLLLEVDPAMKNVEFKAQKRGCLCTVHREADFFWSLCTADMSSLE 300
 DB 241 FFIQNVVSDGQLEDSSLLLEVDPAMKNVEFKAQKRGCLCTVHREADFFWSLCTADMSSLE 300
 QY 301 QSHSSPSLYLQCLSQKLRQERTIPGSGITESKDMHFSSLGICILLDVL 348
 DB 301 QSHSSPSLYLQCLSQKLRQERTIPGSGITESKDMHFSSLGICILLDVL 348

RESULT 2
 ADA10619

ID ADA10619 standard; protein; 348 AA.

XX

AC ADA10619;

XX

DT 06-NOV-2003 (first entry)

XX Human inhibitor of FLICE (I-FLICE-2) protein.

DE

XX Human; I-FLICE-2; inhibitor of FLICE; FADD-like ICE;
 XX tumour necrosis factor receptor-1 inhibitor; TNFR-1 inhibitor;
 KW CD-95 induced apoptosis; apoptosis associated disease;
 KW Alzheimer's disease; rheumatoid arthritis; stroke; osteoporosis;
 KW ischaemia; septic shock; degenerative liver disease;
 KW cardiovascular disorder; aberrant cell survival; nootropic;
 KW antirheumatic; vasotropic; hepatotropic; osteopathic; cardiac;
 KW cerebroprotective; antibacterial; antiarthritic; vasodilator.

XX Homo sapiens.

OS

XX US2003087339-A1.

PN

XX

PD 08-MAY-2003.

XX

PF 21-JAN-1998; 98US-00009893.

XX

PR 21-JAN-1997; 97US-0034205P.

PR 05-AUG-1997; 97US-0054800P.

XX (NIJ/) NI J.

PA (ROSE/) ROSEN C A.

PA (DIXI/) DIXIT V M.

PA (GENT/) GENTZ R L.

XX (KENN/) KENNY J J.

PI Ni J, Rosen CA, Dixit VM, Gentz RL, Kenny JJ;

XX WPI; 2003-576674/54.

DR N-PSDB; ADA10618.

XX

PT New I-FLICE-1 (inhibitor of FLICE 1) or I-FLICE-2 nucleic acids, useful
 PT for treating diseases associated with apoptosis e.g., Alzheimer's
 PT disease, rheumatoid arthritis, stroke, osteoporosis, ischemia or septic
 PT shock.

XX Claim 1; Fig 4A-4C; 48pp; English.

XX

CC The present invention relates to the isolation of novel human I-FLICE-1
 CC (inhibitor of FLICE (FADD-like ICE)) and I-FLICE-2 proteins, and the
 CC polynucleotide sequences encoding them. The I-FLICE-1 and I-FLICE-2
 CC proteins are novel inhibitors of tumour necrosis factor receptor-1 (TNFR-
 CC 1) and CD-95 induced apoptosis. Also disclosed are vectors, host cells
 CC and recombinant methods for producing the I-FLICE proteins. The sequences
 CC and methods are useful for treating diseases associated with apoptosis
 CC e.g. Alzheimer's disease, rheumatoid arthritis, stroke, osteoporosis,
 CC ischaemia, septic shock, degenerative liver disease, and cardiovascular
 CC disorders. They are also useful for diagnosing diseases or disorders
 CC associated with aberrant cell survival in an individual. The present
 CC sequence represents human I-FLICE-2.

XX Sequence 348 AA;

Query Match 100.0%; Score 1800; DB 7; Length 348;

Best Local Similarity 100.0%; Pred. No. 1.7e-171;

Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEIGEDLDKSDVSSLIFLMKDYMGRGKISKEKSFLLDVVELEKLNLVAPDQDLLEKCL 60

DB 1 MAEIGEDLDKSDVSSLIFLMKDYMGRGKISKEKSFLLDVVELEKLNLVAPDQDLLEKCL 60

QY 61 KNHRIIDLTKIKYKQSVQAGTGYRNVLAQAIQKSLKDPNNFPREPVKKSIOSEAF 120

DB 61 KNHRIIDLTKIKYKQSVQAGTGYRNVLAQAIQKSLKDPNNFPREPVKKSIOSEAF 120

QY 121 LPQSIPEERYKMKSPGLGICLIIDICIGNETELLRTFTSLGYEVQKFLHLSMHGISOILG 180

DB 121 LPQSIPEERYKMKSPGLGICLIIDICIGNETELLRTFTSLGYEVQKFLHLSMHGISOILG 180

QY 181 QFACMPEDRDYDFVCVLVSRGSGSVGVGDQTHSGPLPHHIRMFMGDSFCPLACKPKM 240

DB 181 QFACMPEDRDYDFVCVLVSRGSGSVGVGDQTHSGPLPHHIRMFMGDSFCPLACKPKM 240

QY 241 FFIQNVVSDGQLEDSSLLLEVDPAMKNVEFKAQKRGCLCTVHREADFFWSLCTADMSSLE 300

DB 241 FFIQNVVSDGQLEDSSLLLEVDPAMKNVEFKAQKRGCLCTVHREADFFWSLCTADMSSLE 300

QY 301 QSHSSPSLYLQCLSQKLRQERTIPGSGITESKDMHFSSLGICILLDVL 348

DB 301 QSHSSPSLYLQCLSQKLRQERTIPGSGITESKDMHFSSLGICILLDVL 348

RESULT 3

ADF76399

ID ADF76399 standard; protein; 348 AA.

XX

AC ADF76399;

XX

DT 26-FEB-2004 (first entry)

XX

DE Novel human secreted and transmembrane protein SeqID 72.

```

181 QFACMPEHRDYDSFVCVLVSRGSSQSYGVNDQTHSGPLHHIRRMFMGDSQCFYLAGKPKM 240
241 FFQNYVYVSGQLEDSSLLVVDGSPAMKNVRFKAQKRGICTVHREADFFWSLCTADMSLLE 300
241 FFQNYVYVSGQLEDSSLLVVDGSPAMKNVRFKAQKRGICTVHREADFFWSLCTADMSLLE 300
301 QSHSSPSLYLQCLSKQLRQERTIPGSGITESKDMHFSSLCILLDVL 348
301 QSHSSPSLYLQCLSKQLRQERTIPGSGITESKDMHFSSLCILLDVL 348

RESULT 4
ADJ96514
ID ID ADJ96514 standard; protein; 348 AA.
XX AC ADJ96514;
XX AC
XX DT
XX DT
XX XX
XX XX
XX XX
XX I-FLICE; FADD-like ICE; apoptosis; Alzheimer's disease;
XX Parkinson's disease; rheumatoid arthritis; septic shock; sepsis; stroke;
XX CNS inflammation; osteoporosis; ischaemia; reperfusion injury;
XX cell death; cardiovascular disease; polycystic kidney disease;
XX liver disease; head injury disease; chromosome mapping; human.
XX OS
XX Homo sapiens.
XX OS
XX US6680171-B1.
XX XX
XX XX
XX XX
XX 20-JAN-2004.
XX XX
XX 21-JAN-2000; 2000US-00489155.
XX PF
XX 21-JAN-1997; 97US-0034205P.
XX PR
XX 05-AUG-1997; 97US-0054800P.
XX PR
XX 21-JAN-1998; 98US-00009893.
XX PR
XX (HUMA-) HUMAN GENOME SCI INC.
XX PA
XX (UNMI ) UNIV MICHIGAN.
XX XX
XX Ni J, Rosen CA, Dixit VM, Gentz RL, Kenny JJ;
XX WPI: 2004-088563/09.
XX DR
XX N-PSDB; ADJ96513.
XX DR
XX
XX New human inhibitor of FADD-like ICE (FLICE) nucleic acids and
XX polypeptides, useful for inhibiting apoptosis for treating e.g.
XX Alzheimer's disease, Parkinson's disease, rheumatoid arthritis, sepsis,
XX ischemia, or stroke.
XX PT
XX Claim 1; SEQ ID NO 6; 58pp; English.
XX PS
XX
XX The present invention relates to novel I-FLICE (FADD-like ICE)-1 and I-
XX FLICE (FADD-like ICE)-2 protein and the polynucleotides encoding them.
XX CC
XX The invention is useful for inhibiting apoptosis and for therapeutic
XX purposes particularly for the treatment of Alzheimer's disease,
XX CC
XX Parkinson's disease, rheumatoid arthritis, septic shock, sepsis, stroke,
XX CC CNS inflammation, osteoporosis, ischaemia, reperfusion injury, cell death,
XX CC associated with cardiovascular disease, polycystic kidney disease,
XX CC apoptosis of endothelial cells in cardiovascular disease, degenerative
XX CC liver disease, MS and head injury disease. The invention is also useful
XX CC in chromosome mapping. The present sequence is human I-FLICE protein.
XX XX
XX Sequence 348 AA;
XX SQ
XX
Query Match 100.0%; Score 1800; DB 8; Length 348;
Best Local Similarity 100.0%; Pred. No. 1.7e-171;
Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY 1 MABIGEDLDKSDVSSLIIFLMKDYMGKGIKSKESFDLWVELEKLNLVAPQDLLEKCL 60

```

```
Db 1 MAEIGEDLDKSDVSSLIIFLMKDYMGGRGKISKESKSFIDLVLVELEKLNLVAPDQDLLEKCL 60
Qy 61 KNHRIIDLTKIKQYKQSQVGAGTSYRNVLQAAIOKSLKDPNNPREPVPKKSIOESEAF 120
Db 61 KNHRIIDLTKIKQYKQSQVGAGTSYRNVLQAAIOKSLKDPNNPREPVPKKSIOESEAF 120
Qy 121 LPQSIPPEERYKMKSKPLGICLIIDICIGNETELLRTDFTTSLGYEVQKFLHLSMHGISIILG 180
Db 121 LPQSIPPEERYKMKSKPLGICLIIDICIGNETELLRTDFTTSLGYEVQKFLHLSMHGISIILG 180
Qy 181 QPACMPEHRDYDSFVCLVSRGSGSVYGVDTQTHSGPLPHHRRMPMGDSCPYLAGKPKM 240
Db 181 QPACMPEHRDYDSFVCLVSRGSGSVYGVDTQTHSGPLPHHRRMPMGDSCPYLAGKPKM 240
Qy 241 FFIQNVVSDGOLEDSSLEVDGPAMKNVEFKAQKRGCTVHREADFFWSLCTADMSSLE 300
Db 241 FFIQNVVSDGOLEDSSLEVDGPAMKNVEFKAQKRGCTVHREADFFWSLCTADMSSLE 300
Qy 301 QSHSSPSLYLQCLSQKLRQERTIPGSGITESKDMHFSSLGICILLDVL 348
Db 301 QSHSSPSLYLQCLSQKLRQERTIPGSGITESKDMHFSSLGICILLDVL 348

RESULT 5
ID ADR11316
XX ADR11316 standard; protein; 348 AA.
AC ADR11316;
XX
DT 23-SEP-2004 (first entry)
DE Human inhibitor of FADD-like ICE-2 (I-FLICE-2) HCEBJ50.
KW human; I-FLICE-2; apoptosis; Alzheimer's disease; Parkinson's disease;
KW rheumatoid arthritis; septic shock; sepsis; stroke; CNS inflammation;
KW osteoporosis; ischaemia; inhibitor of FADD-like ICE-2.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 1..75
FT /note = DED/FADD homology domain
XX
XX US2004121387-A1.
XX
PD 24-JUN-2004.
XX
PF 17-NOV-2003; 2003US-00713208.
XX
PR 21-JAN-1997; 97US-0034205P.
PR 05-AUG-1997; 97US-0054800P.
PR 21-JAN-1998; 98US-00009893.
PR 21-JAN-2000; 2000US-00489155.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA (UNMI ) UNIV MICHIGAN.
XX
PI Ni J, Rosen CA, Dixit VM, Gentz RL, Kenny JJ;
XX
XX WPI; 2004-479673/45.
DR N-PSDB; ADR11315.
XX
XX New I-FLICE-1 or I-FLICE-2 polynucleotides and polypeptides, useful in
PT diagnosing and treating Alzheimer's disease, Parkinson's diseases,
PT rheumatoid arthritis, septic shock, sepsis, stroke, or osteoporosis.
XX
PS Claim 1; SEQ ID NO 6; 52pp; English.
XX
XX The invention relates to an isolated I-FLICE-1 nucleic acid molecule. The
CC polynucleotides and polypeptides, methods, and composition are useful in
CC diagnosing and treating diseases and disorders associated with apoptosis
CC or with aberrant cell survival, e.g. Alzheimer's disease, Parkinson's
```

```
CC diseases, rheumatoid arthritis, septic shock, sepsis, stroke, CNS
CC inflammation, osteoporosis, or ischaemia. The present sequence represents
CC the amino acid sequence of the human inhibitor of FADD-like ICE-2 (I-
CC FLICE-2) HCEBJ50.
XX
SQ Sequence 348 AA;
Query Match 100.0%; Score 1800; DB 8; Length 348;
Best Local Similarity 100.0%; Pred. No. 1.7e-171;
Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAEIGEDLDKSDVSSLIIFLMKDYMGGRGKISKESKSFIDLVLVELEKLNLVAPDQDLLEKCL 60
Db 1 MAEIGEDLDKSDVSSLIIFLMKDYMGGRGKISKESKSFIDLVLVELEKLNLVAPDQDLLEKCL 60
Qy 61 KNHRIIDLTKIKQYKQSQVGAGTSYRNVLQAAIOKSLKDPNNPREPVPKKSIOESEAF 120
Db 61 KNHRIIDLTKIKQYKQSQVGAGTSYRNVLQAAIOKSLKDPNNPREPVPKKSIOESEAF 120
Qy 121 LPQSIPPEERYKMKSKPLGICLIIDICIGNETELLRTDFTTSLGYEVQKFLHLSMHGISIILG 180
Db 121 LPQSIPPEERYKMKSKPLGICLIIDICIGNETELLRTDFTTSLGYEVQKFLHLSMHGISIILG 180
Qy 181 QPACMPEHRDYDSFVCLVSRGSGSVYGVDTQTHSGPLPHHRRMPMGDSCPYLAGKPKM 240
Db 181 QPACMPEHRDYDSFVCLVSRGSGSVYGVDTQTHSGPLPHHRRMPMGDSCPYLAGKPKM 240
Qy 241 FFIQNVVSDGOLEDSSLEVDGPAMKNVEFKAQKRGCTVHREADFFWSLCTADMSSLE 300
Db 241 FFIQNVVSDGOLEDSSLEVDGPAMKNVEFKAQKRGCTVHREADFFWSLCTADMSSLE 300
Qy 301 QSHSSPSLYLQCLSQKLRQERTIPGSGITESKDMHFSSLGICILLDVL 348
Db 301 QSHSSPSLYLQCLSQKLRQERTIPGSGITESKDMHFSSLGICILLDVL 348

RESULT 6
AA05788
ID AA05788 standard; protein; 366 AA.
XX
AC AA05788;
XX
DT 02-AUG-1999 (first entry)
DE Human MACH related inducer of toxicity MRIT alpha 2.
XX
KW MRIT alpha 2; MACH related inducer of toxicity; human; apoptosis;
KW anti-apoptotic; cancer; autoimmune disease; angiogenesis;
KW atherosclerosis; neurodegenerative disease; Alzheimer's disease;
KW Parkinson's disease; retinitis pigmentosa; stroke; AIDS; infection;
KW aplastic anaemia; myocardial infarction; therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Active-site 262..266
XX
XX WO9918230-A2.
XX
PD 15-APR-1999.
XX
XX 07-OCT-1998; 98WO-US021132.
XX
XX 07-OCT-1997; 97US-00946226.
XX
XX (UNIW ) UNIV WASHINGTON.
PI Chaudhary PM;
XX
XX WPI; 1999-277275/23.
DR N-PSDB; AAX25509.
XX
XX Identifying regulators of MACH-related inducer of toxicity.
FT
```


ADRI14101;
 21-OCT-2004 (first entry)
 Human NF-kappaB pathway-associated protein SeqID102.
 NF-kappaB pathway; antiinflammatory; cytostatic; hepatotropic; virucide;
 antiarthritic; antirheumatic; gastrointestinal-Gen; antiasthmatic;
 antitartarosclerotic; immunomodulator; cerebroprotective; vasotropic;
 immunosuppressive; vulnary; gene therapy; immune disorder;
 inflammatory disorder; NF-kappaB regulation; cancer; aberrant apoptosis;
 hepatic disorder; Hodgkin's lymphoma; haematopoietic tumour;
 hyper-IgM syndrome; hypohidrotic ectodermal dysplasia;
 X-linked anhidrotic ectodermal dysplasia;
 viral infection; HIV-1; HTLV-1; hepatitis B; hepatitis C; EBV; influenza;
 viral replication; host cell survival; evasion of immune response;
 rheumatoid arthritis; inflammatory bowel disease; colitis; asthma;
 atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAE;
 autoimmune disorder; hyper immune activity;
 aberrant acute phase response; hypercongenital condition; birth defect;
 necrotic lesion; wound; organ transplant rejection;
 aberrant signal transduction; proliferating disorder; cancer;
 HIV propagation; human.
 Homo sapiens.
 WO2004065577-A2.
 05-AUG-2004.
 13-JAN-2004; 2004WO-US000798.
 14-JAN-2003; 2003US-0440068P.
 12-MAY-2003; 2003US-0469757P.
 (BRIM) BRISTOL-MYERS SQUIBB CO.
 Nadler SG, Neubauer MG, Feder JN, Carman J;
 WPI: 2004-562168/54.
 N-PSDB; ADRI14100.
 New isolated polynucleotides and polypeptides associated with NF-kappaB
 pathway, useful for diagnosing, treating, or preventing disorders or
 diseases associated with NF-kappaB pathway.
 Claim 6; SEQ ID NO 102; 237pp; English.
 This invention relates to the novel association of protein sequences (and
 the genes which encode them) to the NF-kappaB pathway. The invention may
 be useful for the production of compounds with an antiinflammatory,
 cytostatic, hepatotropic, virucide, antiarthritic, antirheumatic,
 gastrointestinal-gen, antiasthmatic, antitartarosclerotic,
 immunomodulator, cerebroprotective, vasotropic, immunosuppressive or
 vulnary activity or for gene therapy. The proteins and nucleotides are
 useful for diagnosing, preventing, treating, or ameliorating conditions
 or diseases associated with the NF-kappaB pathway. The condition is an
 immune disorder, an inflammatory disorder, an inflammatory disorder
 related to aberrant NF-kappaB regulation, cancer, aberrant apoptosis,
 hepatic disorders, Hodgkin's lymphomas, haematopoietic tumours, hyper-IgM
 syndromes, hypohidrotic ectodermal dysplasia, X-linked anhidrotic
 ectodermal dysplasia, immunodeficiency, viral infections, HIV-1, HTLV-1,
 hepatitis B, hepatitis C, EBV, influenza, viral replication, host cell
 survival, evasion of immune responses, rheumatoid arthritis, inflammatory
 bowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick
 syndrome, stroke, EAE, autoimmune disorders, disorders related to hyper
 immune activity, disorders related to aberrant acute phase responses,
 hypercongenital conditions, birth defects, necrotic lesions, wounds,
 organ transplant rejection, conditions related to organ transplant
 rejection, disorders related to aberrant signal transduction,
 proliferating disorders, cancers and HIV propagation in cells infected
 with other viruses. The present sequence is that of a human protein which
 is subject to the novel association with the NF-kappaB pathway of the

CC invention. Note: This sequence does not appear in the specification but
 CC was obtained by the indexer from Genbank.
 XX
 SQ Sequence 462 AA;
 Query Match 98.6%; Score 1774; DB 8; Length 462;
 Best Local Similarity 94.5%; Pred. No. 1e-168;
 Matches 346; Conservative 2; Mismatches 0; Indels 18; Gaps 1;
 QY 1 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKEKSFLLDVLVELEKLNLVAPDQLLEKCL 60
 DB 97 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKEKSFLLDVLVELEKLNLVAPDQLLEKCL 156
 QY 61 KNIHRIDLTKTIQKYQSQVAGTSYRNVLQAAIQKSLKDPNNFR----- 106
 DB 157 KNIHRIDLTKTIQKYQSQVAGTSYRNVLQAAIQKSLKDPNNFRLLHNGRSKEQRLKEQ 216
 QY 107 ----BEPVKYSIQSEAFLPQSIPEERYKMSKPLIGICLIIDICINETELLDRDTTSLGY 162
 DB 217 LGAQQEPVKYSIQSEAFLPQSIPEERYKMSKPLIGICLIIDICINETELLDRDTTSLGY 276
 QY 163 EVOKELHLSMHGISOILGQFACMPHEDYDSFVCLVSRGGSQSVYGVDTHTSGPLHHI 222
 DB 277 EVOKELHLSMHGISOILGQFACMPHEDYDSFVCLVSRGGSQSVYGVDTHTSGPLHHI 336
 QY 223 RRMFMGDCPYLAGPKPMFFIYVYVSDGQLEDSSILLEVDGPMKNVFKAKRGICLVH 282
 DB 337 RRMFMGDCPYLAGPKPMFFIYVYVSDGQLEDSSILLEVDGPMKNVFKAKRGICLVH 396
 QY 283 READFFWSLCTADMSLLEQSHSSPSLYLQCLSQKLQERGTIPGSGITESKDMHFSSLGC 342
 DB 397 READFFWSLCTADMSLLEQSHSSPSLYLQCLSQKLQERGTIPGSGITESKDMHFSSLGC 456
 QY 343 ILLDVL 348
 DB 457 ILLDVL 462
 RESULT 9
 ID AAY05791 standard; protein; 384 AA.
 XX
 AC AAY05791;
 XX
 DT 02-AUG-1999 (first entry)
 XX
 DE MRIT alpha 3 polypeptide.
 XX
 KW MRIT alpha 3; MACH related inducer of toxicity; human; apoptosis;
 KW anti-apoptotic; cancer; autoimmune disease; angiogenesis;
 KW atherosclerosis; neurodegenerative disease; Alzheimer's disease;
 KW Parkinson's disease; retinitis pigmentosa; stroke; AIDS; infection;
 KW aplastic anaemia; myocardial infarction; therapy; mutant.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO9918230-A2.
 XX
 PD 15-APR-1999.
 XX
 PF 07-OCT-1998; 98WO-US021132.
 XX
 PR 07-OCT-1997; 97US-00946226.
 XX
 PA (UNITW) UNIV WASHINGTON.
 XX
 PI Chaudhary PM;
 XX
 DR WPI; 1999-277275/23.
 XX
 PT Identifying regulators of MACH-related inducer of toxicity.
 XX

```
PS Example 2; Page; 78pp; English.
XX
CC The present sequence represents MRIT alpha 3, comprising amino acid
CC residues 97-480 of novel human MACH-related inducer of toxicity MRIT
CC alpha 1 (see AY05787). This deletion mutant was used to examine the
CC interaction of MRIT alpha 1 with caspases. The results indicated that
CC FLICE-p20 binding to MRIT alpha 1 does not require the N-terminal 96
CC amino acids. The invention provides multiple isoforms of MRIT (see
CC AY05787-89), isolated active fragments of which have either pro-
CC apoptotic or anti-apoptotic activity. Selective enhancers and inhibitors
CC of MRIT apoptotic activity can be identified and used to treat diseases
CC mediated by the dysfunction of programmed cell death or proliferation,
CC such as cancer or a neurodegenerative disorder. Note: the present
CC sequence is not shown in the specification but is derived from the MRIT
CC alpha 1 sequence given in figure 1F
XX
SQ Sequence 384 AA;
Query Match 90.8%; Score 1635; DB 2; Length 384;
Best Local Similarity 94.1%; Pred. No. 7.1e-155;
Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;
QY 1 MAEIGEDLDKSDVSSLIFLMKDYMGRGKISKESFLDLVVELEKLNVLVAPDQDLLEKCL 60
DB 1 MAEIGEDLDKSDVSSLIFLMKDYMGRGKISKESFLDLVVELEKLNVLVAPDQDLLEKCL 60
QY 61 KNIHRIDLTKTKQYKQSVQAGTSYRNVLQAAIQKSLKDPNNFR----- 106
DB 61 KNIHRIDLTKTKQYKQSVQAGTSYRNVLQAAIQKSLKDPNNFR----- 106
QY 107 ----EPPVKKSTQESFAFLPQSIPEERYKMKSKPLGICLIIDCIGNETELLRTFTSLGY 162
DB 121 LGAQQEPVKKSTQESFAFLPQSIPEERYKMKSKPLGICLIIDCIGNETELLRTFTSLGY 180
QY 163 EVQKFLHLSMHGISOILGQFACMPHEHDYDSFVCLVSRGGSQSVGVVDQTHSGPLPHHI 222
DB 181 EVQKFLHLSMHGISOILGQFACMPHEHDYDSFVCLVSRGGSQSVGVVDQTHSGPLPHHI 240
QY 223 RRMFMGDCSPYLAGPKPMFFIQNYVVDGQLEDSSLLVEDGPMKNVFEKAKRGGLCTVH 282
DB 241 RRMFMGDCSPYLAGPKPMFFIQNYVVDGQLEDSSLLVEDGPMKNVFEKAKRGGLCTVH 300
QY 283 READPFWSLCTADMSLLEQSHSSPSLYLOCLSQKLRQER 321
DB 301 READPFWSLCTADMSLLEQSHSSPSLYLOCLSQKLRQER 339
RESULT 10
AAW58578
ID AAW58578 standard; protein; 480 AA.
XX
AC AAW58578;
XX
DT 07-SEP-1998 (first entry)
XX
DE Human FIN-1.
XX
KW Human; FIN-1; FLICE inhibitor-1; ICE-LAP7; death effector domain; DRD;
KW apoptosis-related protein; caspase; viral infection; cancer; tumour;
KW diagnosis; ischaemic injury; neuro-degenerative disorder.
XX
OS Homo sapiens.
XX
PN EP841399-A2.
XX
PD 13-MAY-1998.
XX
PF 10-NOV-1997; 97EP-00309003.
XX
PR 12-NOV-1996; 96US-00748086.
XX
PA (SMIK ) SMITHKLINE BEECHAM CORP.
XX
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```
PI Kikly K, Emery JG;
XX
DR WPI; 1998-252943/23.
DR N-PSDB; AAV311375.
XX
PT New nucleic acid encoding human apoptosis-related protein - used for
PT diagnosis and treatment of e.g. viral infections, tumour, ischaemic
PT injury and neuro-degenerative disorders.
XX
PS Claim 11; Page 25-27; 48pp; English.
XX
CC The present sequence represents human FIN-1 (FLICE inhibitor-1), which is
CC a caspase. FLICE (ICE-LAP7) is a protease of the interleukin-converting
CC enzyme family, a protein involved in the regulation of cell death. A host
CC cell, comprising a vector containing the FIN-1 encoding DNA, can be used to
CC produce FIN-1. The vector containing the DNA can be used for producing a
CC cell which expresses a polypeptide by transforming or transfecting the
CC cell with it so that the cell expresses the polypeptide encoded the human
CC cDNA contained in the vector. The polypeptide or its antagonist can be
CC used in the treatment of patients needing FIN-1 by in-vivo
CC administration. Conditions which may be treated include viral infection,
CC tumours (especially solid tumours), ischaemic injury (e.g. stroke or
CC myocardial infarction), neurodegenerative disorders (e.g. Alzheimer's or
CC Parkinson's disease), osteoporosis, osteoarthritis, polycystic kidney
CC disease, chronic degenerative liver disease, acquired immunodeficiency
CC syndrome (AIDS) and aplastic anaemia. The polynucleotides may also be
CC used for chromosome identification
XX
SQ Sequence 480 AA;
Query Match 90.8%; Score 1635; DB 2; Length 480;
Best Local Similarity 94.1%; Pred. No. 9.9e-155;
Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;
QY 1 MAEIGEDLDKSDVSSLIFLMKDYMGRGKISKESFLDLVVELEKLNVLVAPDQDLLEKCL 60
DB 97 MAEIGEDLDKSDVSSLIFLMKDYMGRGKISKESFLDLVVELEKLNVLVAPDQDLLEKCL 156
QY 61 KNIHRIDLTKTKQYKQSVQAGTSYRNVLQAAIQKSLKDPNNFR----- 106
DB 157 KNIHRIDLTKTKQYKQSVQAGTSYRNVLQAAIQKSLKDPNNFR----- 216
QY 107 ----EPPVKKSTQESFAFLPQSIPEERYKMKSKPLGICLIIDCIGNETELLRTFTSLGY 162
DB 217 LGAQQEPVKKSTQESFAFLPQSIPEERYKMKSKPLGICLIIDCIGNETELLRTFTSLGY 276
QY 163 EVQKFLHLSMHGISOILGQFACMPHEHDYDSFVCLVSRGGSQSVGVVDQTHSGPLPHHI 222
DB 277 EVQKFLHLSMHGISOILGQFACMPHEHDYDSFVCLVSRGGSQSVGVVDQTHSGPLPHHI 336
QY 223 RRMFMGDCSPYLAGPKPMFFIQNYVVDGQLEDSSLLVEDGPMKNVFEKAKRGGLCTVH 282
DB 337 RRMFMGDCSPYLAGPKPMFFIQNYVVDGQLEDSSLLVEDGPMKNVFEKAKRGGLCTVH 396
QY 283 READPFWSLCTADMSLLEQSHSSPSLYLOCLSQKLRQER 321
DB 397 READPFWSLCTADMSLLEQSHSSPSLYLOCLSQKLRQER 435
RESULT 11
AAW69715
ID AAW69715 standard; protein; 480 AA.
XX
AC AAW69715;
XX
DT 24-NOV-1998 (first entry)
XX
DE Human Casper protein.
XX
KW Casper; caspase-eight-related protein; human; apoptosis.
XX
OS Homo sapiens.
XX
```


PN WO9833883-A1.
XX
PD 06-AUG-1998.
XX
PF 05-FEB-1998; 98WO-US002117.
XX
PR 05-FEB-1997; 97US-00795088.
XX
PA (TULA-) TULARIK INC.
XX
PI Shu H, Goeddel DV;
XX
DR WPI; 1998-437440/37.
XX
DR N-PSDB; AAV50436.
XX
PT New Casper protein involved in regulation of apoptosis - used, e.g. to
PT identify specific modulators, identify or isolate similar sequences and
PT in gene therapy.
XX
PS Claim 1; Page 22-23; 29pp; English.
XX
CC This is the amino acid sequence of a novel human protein, designated
CC Casper (for caspase-eight-related protein), that is involved in
CC regulation of apoptosis. The sequence is deduced from an isolated cDNA
CC clone (see AAV50436). Casper protein interacts with FADD and is recruited
CC to Fas. It also interacts with caspase-8 and caspase-3, and with TRAF1
CC and TRAF2. A claimed isolated polypeptide comprises the full-length
CC Casper amino acid sequence, or a fragment of at least 6 consecutive amino
CC acid residues including at least one of residues 1-96, 1-202, 1-435, 78-
CC 480, 192-480, 390-480 or residue 360. The isolated protein, or cells that
CC express the protein, can be used to screen for agents, e.g. antibodies or
CC T-cell receptors, that specifically modify the binding of Casper to a
CC target, and thus its function
XX
SQ Sequence 480 AA;

Query Match 90.8%; Score 1635; DB 2; Length 480;
Best Local Similarity 94.1%; Pred. No. 9.9e-155;
Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;

QY 1 MAEIGEDLDKSDVSSLIIFLMKDYMGKGKISKEKSFIDLIVVELEKLNLVAPDQDLLEKCL 60
DB 97 MAEIGEDLDKSDVSSLIIFLMKDYMGKGKISKEKSFIDLIVVELEKLNLVAPDQDLLEKCL 156

QY 61 KNIHRIDLTKTKIQKYKQSVQAGTGYRNVLQAAIQKSLKDPNNFR----- 106
DB 157 KNIHRIDLTKTKIQKYKQSVQAGTGYRNVLQAAIQKSLKDPNNFHLNGRSKEQRLKEQ 216

QY 107 ----EPPVKKSIOESAEFLPQSIPEERYKMKSKPLGICLIIDICIGNETELLRDFTTSLGY 162
DB 217 LGAQQEPVKKSIQESAEFLPQSIPEERYKMKSKPLGICLIIDICIGNETELLRDFTTSLGY 276

QY 163 EVQKFLHLSMHGSIQILGQFACMPHRDYSFVCLVSRGSGSVYGVVDQTHSGPLHHI 222
DB 277 EVQKFLHLSMHGSIQILGQFACMPHRDYSFVCLVSRGSGSVYGVVDQTHSGPLHHI 336

QY 223 RRMFMGDSCPYLAGKPKMFQIYNYVSDGLEDSLSLEVDGPMKNVFEKAKRGKLCVTH 282
DB 337 RRMFMGDSCPYLAGKPKMFQIYNYVSEGLEDSLSLEVDGPMKNVFEKAKRGKLCVTH 396

QY 283 READTFWSLCTADMSLLEQSHSSPSLYLQCLSKQLRQR 321
DB 397 READTFWSLCTADMSLLEQSHSSPSLYLQCLSKQLRQR 435

RESULT 12
ID AAW69229
XX AAW69229 standard; protein; 480 AA.
AC AAW69229;
XX
DT 16-OCT-1998 (first entry)
XX

DE I-FLICE-1 protein.
XX
KW I-FLICE-1; FADD like ICE protein; inhibitor; TNFR-1; Alzheimer's disease;
KW CD-95 induced apoptosis; Parkinson's disease; rheumatoid arthritis;
KW CNS inflammation; osteoporosis; ischaemia; polycystic kidney disease;
KW multiple sclerosis; head injury; cancer; autoimmune disorder; therapy;
KW viral infection; graft versus host disease; graft rejection.
XX
OS Homo sapiens.
XX
PN WO9831801-A1.
XX
PD 23-JUL-1998.
XX
PF 21-JAN-1998; 98WO-US000969.
XX
PR 21-JAN-1997; 97US-0034205P.
PR 05-AUG-1997; 97US-0054800P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (UNMI) UNIV MICHIGAN.
XX
PI Ni J, Rosen CA, Dixit VM, Gentz RL, Kenny JJ;
XX
DR WPI; 1998-414100/35.
DR N-PSDB; AAV44806.
XX
PT New inhibitory polypeptides of FLICE - used to develop products for
PT treating e.g. Alzheimer's disease, sepsis, stroke, osteoporosis, cancers,
PT autoimmune disorders, viral infection or graft rejection.
XX
PS Claim 9; Fig 1; 118pp; English.
XX
CC This sequence is an inhibitor of Fas-ligand associated with death
CC domain (FADD) like ICE (I-FLICE) protein, designated I-FLICE-1. The
CC proteins can inhibit both TNFR-1 and CD-95 induced apoptosis. These are
CC the first examples of a naturally occurring catalytically inactive
CC caspase that can act as a dominant negative inhibitor of apoptosis. The
CC polypeptides and agonists can be used for treating e.g. Alzheimer's
CC disease, Parkinson's disease, rheumatoid arthritis, septic shock, sepsis,
CC stroke, CNS inflammation, osteoporosis, ischaemia, reperfusion injury,
CC cell death associated with cardiovascular disease, polycystic kidney
CC disease, apoptosis of endothelial cells in cardiovascular disease,
CC degenerative liver disease, multiple sclerosis (MS) and head injury
CC damage. Antagonists of the polypeptides can be used for treating cancers
CC (e.g. follicular lymphomas, carcinomas with p53 mutations, hormone-
CC dependent tumours, and cancers of the breast, ovary, prostate, bone,
CC liver, lung, pancreas, and spleen), autoimmune disorders (e.g. systemic
CC lupus erythematosus, immune-related glomerulonephritis, rheumatoid
CC arthritis), and viral infections (e.g. herpes viruses, pox viruses and
CC adenoviruses), graft versus host disease, acute disease, acute graft
CC rejection, and chronic graft rejection. The products can also be used for
CC detection, diagnosis and drug screening
XX
SQ Sequence 480 AA;

Query Match 90.8%; Score 1635; DB 2; Length 480;
Best Local Similarity 94.1%; Pred. No. 9.9e-155;
Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;

QY 1 MAEIGEDLDKSDVSSLIIFLMKDYMGKGKISKEKSFIDLIVVELEKLNLVAPDQDLLEKCL 60
DB 97 MAEIGEDLDKSDVSSLIIFLMKDYMGKGKISKEKSFIDLIVVELEKLNLVAPDQDLLEKCL 156

QY 61 KNIHRIDLTKTKIQKYKQSVQAGTGYRNVLQAAIQKSLKDPNNFR----- 106
DB 157 KNIHRIDLTKTKIQKYKQSVQAGTGYRNVLQAAIQKSLKDPNNFHLNGRSKEQRLKEQ 216

QY 107 ----EPPVKKSIOESAEFLPQSIPEERYKMKSKPLGICLIIDICIGNETELLRDFTTSLGY 162
DB 217 LGAQQEPVKKSIQESAEFLPQSIPEERYKMKSKPLGICLIIDICIGNETELLRDFTTSLGY 276

QY 163 EVQKFLHLSMHGSIQILGQFACMPHRDYSFVCLVSRGSGSVYGVVDQTHSGPLHHI 222


```
Db 277 EVQKFLHLSMHGSIQLGQFACMPHRDYDSFVCVLVSRGSGSVYGVDTHTSGLPLHHI 336
QY 223 RRMFMGDSCPYLAKGPKMPFFIQNYVVSQDQEDSSLLLEVDGPMKNVFEKAKRGGLCTVH 282
Db 337 RRMFMGDSCPYLAKGPKMPFFIQNYVVSQDQEDSSLLLEVDGPMKNVFEKAKRGGLCTVH 396
QY 283 READPFWSLCTADMSLLEQSHSPSLYLQCLSQKROER 321
Db 397 READPFWSLCTADMSLLEQSHSPSLYLQCLSQKROER 435

RESULT 13
AAW76631
ID AAW76631 standard; protein; 480 AA.
XX
AC AAW76631;
XX
DT 12-JUL-1999 (first entry)
XX
DE Human CFLIP-L protein.
XX
KW Death effector domain; human; murine; anti-apoptotic; treatment;
KW HIV infection; autoimmune disease; FLIP protein.
XX
OS Homo sapiens.
XX
PN DE19713393-A1.
XX
PD 08-OCT-1998.
XX
PF 01-APR-1997; 97DE-01013393.
XX
PR 01-APR-1997; 97DE-01013393.
XX
PA (TSCH/) TSCHOPP J.
PI Tschopp J, Thome M, Burns K, Irmeler M, Hahne M, Schroeter M;
PI Schneider P, Bodmer J, Steiner V, Rimoldi D, Hoffmann K, French EL;
XX
DR WPI; 1998-532710/46.
DR N-PSDB; AAV61937.
PT New DNA encoding for anti-apoptotic gene product - used to treat HIV
PT infections and autoimmune diseases.
XX
PS Claim 20; Fig 4B; 45pp; German.
XX
CC This invention describes novel human and mouse anti-apoptotic gene
CC products which contain at least one death effector domain. The products
CC of the invention are used in the treatment of HIV infections and
CC autoimmune diseases
XX
SQ Sequence 480 AA;

Query Match 90.8%; Score 1635; DB 2; Length 480;
Best Local Similarity 94.1%; Pred. No. 9.9e-155;
Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;

QY 1 MAEIGDLDKSDVSSLIFLMKDYMGRGKISKESFLDLVVELEKLNVLAPDQDLLEKCL 60
Db 97 MAEIGDLDKSDVSSLIFLMKDYMGRGKISKESFLDLVVELEKLNVLAPDQDLLEKCL 156
QY 61 KNHRIIDLTKIKYKQSQVQAGTSYRNVLQAAIQSLKDPGNNFR----- 106
Db 157 KNHRIIDLTKIKYKQSQVQAGTSYRNVLQAAIQSLKDPGNNFELNGRSKEQRLKEQ 216
QY 107 -----EPVKVKSQESAFIPQSIPEERYKMKSPGLGICLIIDICIGNETELLDRDTFTSLGY 162
Db 217 LGAQKPEPVKKSQESAFIPQSIPEERYKMKSPGLGICLIIDICIGNETELLDRDTFTSLGY 276
QY 163 EVQKFLHLSMHGSIQLGQFACMPHRDYDSFVCVLVSRGSGSVYGVDTHTSGLPLHHI 222
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```
Db 277 EVQKFLHLSMHGSIQLGQFACMPHRDYDSFVCVLVSRGSGSVYGVDTHTSGLPLHHI 336
QY 223 RRMFMGDSCPYLAKGPKMPFFIQNYVVSQDQEDSSLLLEVDGPMKNVFEKAKRGGLCTVH 282
Db 337 RRMFMGDSCPYLAKGPKMPFFIQNYVVSQDQEDSSLLLEVDGPMKNVFEKAKRGGLCTVH 396
QY 283 READPFWSLCTADMSLLEQSHSPSLYLQCLSQKROER 321
Db 397 READPFWSLCTADMSLLEQSHSPSLYLQCLSQKROER 435

RESULT 14
AAV05787
ID AAV05787 standard; protein; 480 AA.
XX
AC AAV05787;
XX
DT 02-AUG-1999 (first entry)
XX
DE Human MACH related inducer of toxicity MRIT alpha 1.
XX
KW MRIT alpha 1; MACH related inducer of toxicity; human; apoptosis;
KW pro-apoptotic; cancer; autoimmune disease; infection; angiogenesis;
KW atherosclerosis; neurodegenerative disease; Alzheimer's disease;
KW Parkinson's disease; retinitis pigmentosa; stroke; AIDS;
KW aplastic anaemia; myocardial infarction; therapy.
XX
OS Homo sapiens.
XX
FH Key
FT Region 1..165
FT Region /note= "death effector domain homology region"
FT Region 140..178
FT Region /note= "Bcl-2 homology region"
FT Region 196..228
FT Region /note= "Bcl-2 homology region"
FT Region 258..289
FT Region /note= "Bcl-2 homology region"
FT Region 299..350
FT Region /note= "Bcl-2 homology region"
FT Region 301..480
FT Region /note= "caspase homology region"
FT Region 356..397
FT Region /note= "Bcl-2 homology region"
FT Active-site 358..362
XX
PN WO9918230-A2.
XX
PD 15-APR-1999.
XX
PF 07-OCT-1998; 98WO-US021132.
XX
PR 07-OCT-1997; 97US-00946226.
XX
PA (UNIW ) UNIV WASHINGTON.
XX
PI Chaudhary PM;
XX
DR WPI; 1999-277275/23.
XX N-PSDB; AAX25508.
PT Identifying regulators of MACH-related inducer of toxicity.
XX
PS Example 1; Fig 1F; 78pp; English.
XX
CC The present sequence represents novel human MACH-related inducer of
CC toxicity (MRIT) isoform MRIT alpha 1, a CED-4 homologue that interacts
CC simultaneously with caspases and Bcl-2 family polypeptides, and which has
CC pro-apoptotic activity. Multiple isoforms of MRIT have been identified,
CC some of which function to induce caspase dependent apoptosis in mammalian
CC cells, e.g. MRIT alpha 1 and MRIT beta 1 (see AAY05789), while others
CC have anti-apoptotic activity, e.g. MRIT alpha 2 (see AAY05788). MRIT
CC alpha 1 includes an N-terminal death effector domain and a C-terminal
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CC caspase homology domain, but is not a cysteine protease. Selective
CC enhancers and inhibitors of MRIT apoptotic activity can be identified and
CC used to treat diseases mediated by the dysfunction of programmed cell
CC death or proliferation. A cell accumulation disorder such as cancer,
CC autoimmune disease, viral infection, angiogenesis or atherosclerosis is
CC treated by administering an agent that selectively enhances MRIT
CC apoptotic activity, thereby inducing apoptosis in a subject. A disorder
CC of cell loss, such as a neurodegenerative disorder, including Alzheimer's
CC disease, Parkinson's disease, retinitis pigmentosa, stroke, aplastic
CC anaemia, myocardial infarction or AIDS can be treated by administering an
CC agent that selectively inhibits MRIT apoptotic activity

XX Sequence 480 AA;

Query Match 90.8%; Score 1635; DB 2; Length 480;
Best Local Similarity 94.1%; Pred. No. 9.9e-155;
Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;
QY 1 MAEIGEDLDKSDVSSLIIFLMKDYMGGRGKISKEKSFLLDLVVELEKLNVLVAPDQDLLEKCL 60
DB 97 MAEIGEDLDKSDVSSLIIFLMKDYMGGRGKISKEKSFLLDLVVELEKLNVLVAPDQDLLEKCL 156
QY 61 KNIHRIDLTKTKQYKQSVQAGTSYRNVLQAAIQKSLKDPNNFR----- 106
DB 157 KNIHRIDLTKTKQYKQSVQAGTSYRNVLQAAIQKSLKDPNNFR----- 216
QY 107 ----BEPVKKSQESAEFLPQSIPEERYKMKSPKIGICLIIDCIGNETELLRTFTSLGY 162
DB 217 LGAQOEPVKKSQESAEFLPQSIPEERYKMKSPKIGICLIIDCIGNETELLRTFTSLGY 276
QY 163 EVQKFLHLSMHGISQILGQFACMPHEHDYDSFVCLVSRGSGSVYGVDTHTSGPLPHHI 222
DB 277 EVQKFLHLSMHGISQILGQFACMPHEHDYDSFVCLVSRGSGSVYGVDTHTSGPLPHHI 336
QY 223 RRMFMGDCPCYLAGKPKMFFIQNYVVSQGLDSSLLLEVDPAMKNVEFKAKRGICLTVH 282
DB 337 RRMFMGDCPCYLAGKPKMFFIQNYVVSQGLDSSLLLEVDPAMKNVEFKAKRGICLTVH 396
QY 283 READFFWSLCTADMSLLEQSHSPSLYLQCLSQKLRQER 321
DB 397 READFFWSLCTADMSLLEQSHSPSLYLQCLSQKLRQER 435

RESULT 15

AA57454

ID AA57454 standard; protein; 480 AA.

XX AC AA57454;

XX DT 25-FEB-2000 (first entry)

XX DE Human FLICE-like inhibitory protein long form protein sequence.

XX KW Human; FLICE-like inhibitory protein long form; FLIP-L; FLIP-S;

XX KW FLICE-like inhibitory protein short form; apoptosis inhibitor;

XX KW arteriosclerosis; vascular wall inflammation; vascular injury;

XX KW Fas ligand-mediated apoptosis; atherosclerosis; transplant.

XX OS Homo sapiens.

XX PN WO9942570-A1.

XX PD 26-AUG-1999.

XX PF 19-FEB-1999; 99WO-US003558.

XX PR 20-FEB-1998; 98US-0075471P.

XX PA (SELI-) ST ELIZABETH'S MEDICAL CENT BOSTON INC.

XX PI Walsh K;

XX DR WPI; 1999-527469/44.

DR N-PSDB; AA239040.

XX Treating conditions characterized by vascular wall inflammation.

XX Claim 5; Page 69-71; 105pp; English.

XX The present sequence represents human FLICE-like inhibitory protein long

CC form, designated FLIP-L. The present invention describes a new treatment

CC of a condition characterised by vascular wall inflammation in a subject

CC comprising administering a FLIP molecule to inhibit Fas ligand-mediated

CC apoptosis of vascular endothelial cells in the subject. The method can be

CC used to treat atherosclerosis, transplant arteriosclerosis and vascular

CC injury

XX Sequence 480 AA;

Query Match 90.8%; Score 1635; DB 2; Length 480;

Best Local Similarity 94.1%; Pred. No. 9.9e-155;

Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;

QY 1 MAEIGEDLDKSDVSSLIIFLMKDYMGGRGKISKEKSFLLDLVVELEKLNVLVAPDQDLLEKCL 60

DB 97 MAEIGEDLDKSDVSSLIIFLMKDYMGGRGKISKEKSFLLDLVVELEKLNVLVAPDQDLLEKCL 156

QY 61 KNIHRIDLTKTKQYKQSVQAGTSYRNVLQAAIQKSLKDPNNFR----- 106

DB 157 KNIHRIDLTKTKQYKQSVQAGTSYRNVLQAAIQKSLKDPNNFR----- 216

QY 107 ----BEPVKKSQESAEFLPQSIPEERYKMKSPKIGICLIIDCIGNETELLRTFTSLGY 162

DB 217 LGAQOEPVKKSQESAEFLPQSIPEERYKMKSPKIGICLIIDCIGNETELLRTFTSLGY 276

QY 163 EVQKFLHLSMHGISQILGQFACMPHEHDYDSFVCLVSRGSGSVYGVDTHTSGPLPHHI 222

DB 277 EVQKFLHLSMHGISQILGQFACMPHEHDYDSFVCLVSRGSGSVYGVDTHTSGPLPHHI 336

QY 223 RRMFMGDCPCYLAGKPKMFFIQNYVVSQGLDSSLLLEVDPAMKNVEFKAKRGICLTVH 282

DB 337 RRMFMGDCPCYLAGKPKMFFIQNYVVSQGLDSSLLLEVDPAMKNVEFKAKRGICLTVH 396

QY 283 READFFWSLCTADMSLLEQSHSPSLYLQCLSQKLRQER 321

DB 397 READFFWSLCTADMSLLEQSHSPSLYLQCLSQKLRQER 435

Search completed: June 20, 2005, 13:02:20

Job time : 170 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 20, 2005, 13:02:28 ; Search time 162 Seconds
(without alignments)
824.845 Million cell updates/sec

Title: US-10-713-208-6

Perfect score: 1800

Sequence: 1 MAEIGEDLDKDVSSILFLM.....ITKDMHFSSIGCILLDLVL 348

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1714042 seqs, 383979560 residues

Total number of hits satisfying chosen parameters: 1714042

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
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11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
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22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1800	100.0	348	10	US-09-009-893-6 Sequence 6, Appli
2	1800	100.0	348	16	US-10-713-208-6 Sequence 6, Appli
3	1800	100.0	348	16	US-10-370-715B-72 Sequence 72, Appli
4	1774	98.6	462	16	US-10-755-889-102 Sequence 102, App
5	1635	90.8	480	9	US-09-861-270-2 Sequence 2, Appli
6	1635	90.8	480	9	US-09-410-194-11 Sequence 11, Appli
7	1635	90.8	480	9	US-09-410-194-17 Sequence 17, Appli
8	1635	90.8	480	10	US-09-009-893-2 Sequence 2, Appli
9	1635	90.8	480	10	US-09-471-749-1 Sequence 1, Appli
10	1635	90.8	480	16	US-10-713-208-2 Sequence 1, Appli
11	1635	90.8	480	17	US-10-832-218-11 Sequence 11, Appli

12	1635	90.8	480	17	US-10-832-218-17 Sequence 17, Appli
13	1630	90.6	391	9	US-09-764-861-37 Sequence 37, Appli
14	1630	90.6	391	10	US-09-764-861-37 Sequence 37, Appli
15	1630	90.6	391	14	US-10-103-313-318 Sequence 318, App
16	1630	90.6	391	14	US-10-115-928-37 Sequence 37, Appli
17	1630	90.6	480	16	US-10-849-901-2 Sequence 2, Appli
18	1579	87.7	480	16	US-10-408-765A-275 Sequence 275, App
19	1554.5	86.4	445	9	US-09-935-223-2 Sequence 2, Appli
20	1554.5	86.4	445	16	US-10-825-282-44 Sequence 44, Appli
21	1018	56.6	481	9	US-09-410-194-12 Sequence 12, Appli
22	1018	56.6	481	9	US-09-410-194-19 Sequence 19, Appli
23	1018	56.6	481	17	US-10-832-218-12 Sequence 12, Appli
24	1018	56.6	481	17	US-10-832-218-19 Sequence 19, Appli
25	1006.5	55.9	484	13	US-10-005-921-2 Sequence 2, Appli
26	1006.5	55.9	484	16	US-10-849-901-5 Sequence 5, Appli
27	527	29.3	221	9	US-09-410-194-15 Sequence 15, Appli
28	527	29.3	221	9	US-09-410-194-22 Sequence 22, Appli
29	527	29.3	221	16	US-10-849-901-4 Sequence 4, Appli
30	527	29.3	221	16	US-10-832-218-15 Sequence 15, Appli
31	527	29.3	221	17	US-10-832-218-22 Sequence 22, Appli
32	391	21.7	76	9	US-09-864-761-35073 Sequence 35073, A
33	313	17.4	479	9	US-09-410-194-20 Sequence 20, Appli
34	313	17.4	479	10	US-09-851-873-101 Sequence 101, App
35	313	17.4	479	15	US-10-368-438-7 Sequence 7, Appli
36	313	17.4	479	16	US-10-849-901-6 Sequence 6, Appli
37	313	17.4	479	17	US-10-832-218-20 Sequence 20, Appli
38	311.5	17.3	478	10	US-09-009-893-3 Sequence 3, Appli
39	311.5	17.3	478	16	US-10-713-208-3 Sequence 3, Appli
40	305.5	17.0	496	16	US-10-825-282-16 Sequence 16, Appli
41	305.5	17.0	496	17	US-10-488-614-8 Sequence 8, Appli
42	305.5	17.0	496	17	US-10-488-608-7 Sequence 7, Appli
43	304.5	16.9	464	15	US-10-368-438-18 Sequence 18, Appli
44	304.5	16.9	496	15	US-10-232-884-6 Sequence 6, Appli
45	302.5	16.8	496	9	US-09-952-768-4 Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-09-009-893-6
; Sequence 6, Application US/09009893
; Publication No. US20030087339A1

GENERAL INFORMATION:

APPLICANT: NI, JIAN
APPLICANT: ROSEN, CRAIG A.
APPLICANT: DIXIT, VISHVA M.
APPLICANT: GENTZ, REINER L.
APPLICANT: KENNY, JOSEPH J.
TITLE OF INVENTION: 1-FLICE, A NOVEL INHIBITOR OF TUMOR
TITLE OF INVENTION: NECROSIS FACTOR RECEPTOR-1 AND CD-95 INDUCED APOPTOSIS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSER: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: US
ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,893
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,205
FILING DATE: 21-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/054,800

FILING DATE: 05-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0970002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-009-893-6

Query Match
Best Local Similarity 100.0%; Score 1800; DB 10; Length 348;
Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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241 PFIQNVVSDGQLEDSSLLVDGPAKKNVEFKAQKRGCLCTVHREADFFWMSLCTADMSLLE 300
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RESULT 2
US-10-713-208-6
Sequence 6, Application US/10713208
Publication No. US20040121387A1
GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: I-FLICE, A Novel Inhibitor of Tumor Necrosis Factor Receptor-1 and
FILE REFERENCE: PF381C1D1
CURRENT APPLICATION NUMBER: US/10/713,208
CURRENT FILING DATE: 2003-11-17
PRIOR APPLICATION NUMBER: US 09/489,155
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 09/009,893
PRIOR FILING DATE: 1998-01-21
PRIOR APPLICATION NUMBER: US 60/054,800
PRIOR FILING DATE: 1997-08-05
PRIOR APPLICATION NUMBER: US 60/034,205
PRIOR FILING DATE: 1997-01-21
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn version 3.2
SEQ ID NO 6
LENGTH: 348
TYPE: PRT
ORGANISM: Homo sapiens
US-10-713-208-6

Query Match
Best Local Similarity 100.0%; Score 1800; DB 16; Length 348;
Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 1.4e-160;
Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
US-10-370-715B-72
Sequence 72, Application US/10370715B
Publication No. US20040258678A1
GENERAL INFORMATION:
Patent Docket Preview
APPLICANT: BODARY, SARAH C.
APPLICANT: CLARK, HILLARY
APPLICANT: BRISDELL, HUNTE
APPLICANT: JACKMAN, JANET
APPLICANT: SCHOFENFELD, JILL R.
APPLICANT: WILLIAMS, P. MICKEY
APPLICANT: WOOD, WILLIAM I.
APPLICANT: WU, THOMAS D.
TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
FILE REFERENCE: P1948R1-US
CURRENT APPLICATION NUMBER: US/10/370,715B
CURRENT FILING DATE: 2003-02-21
NUMBER OF SEQ ID NOS: 742
SEQ ID NO 72
LENGTH: 348
TYPE: PRT
ORGANISM: Homo sapien
US-10-370-715B-72

Query Match
Best Local Similarity 100.0%; Score 1800; DB 16; Length 348;
Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 241 PFQNYVSDGQLESDSSLEVDGPAKKNVEFKAQKRGCTVHREADFFWSLCTADMSLLE 300
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DB 301 QSHSPSLYLQCLSQKLRQERTIPGSGITGSKDMHFFSLGCLLDVL 348

RESULT 4
US-10-755-889-102
; Sequence 102, Application US/10755889
; Publication No. US20040171823A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF- κ B
; FILE REFERENCE: D0284 NP
; CURRENT APPLICATION NUMBER: US/10/755,889
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: U.S. 60/440,068
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: U.S. 60/469,757
; PRIOR FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 102
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-755-889-102

Query Match 98.6%; Score 1774; DB 16; Length 462;
Best Local Similarity 94.5%; Pred. No. 5.8e-158;
Matches 346; Conservative 2; Mismatches 0; Indels 18; Gaps 1;

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DB 157 KNIHRIDLTKIKQYKQSQVQAGTSYRNVLQAAIOKSLKDPNNFRFLHNGRKEQRLKEQ 216
QY 107 ----BEPVKKSIOESEAFIPQSIPEERYKMSKPLGICLIIDICINETELLRTDFTSLGY 162
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DB 277 EVQKFLHLSMHGISOILGQFACMPHEHRDYSFVCLVSRGGSQSVYGVVDQTHSGPLHHI 336
QY 223 RMFMGDCSPYLAKGPKMFFIQQNYVSDGQLESDSSLEVDGPAKKNVEFKAQKRGCTVH 282
DB 337 RMFMGDCSPYLAKGPKMFFIQQNYVSDGQLESDSSLEVDGPAKKNVEFKAQKRGCTVH 396
QY 283 READFFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQERTIPGSGITGSKDMHFFSLGC 342
DB 397 READFFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQERTIPGSGITGSKDMHFFSLGC 456
QY 343 ILLDVL 348
DB 457 ILLDVL 462

RESULT 5
US-09-861-270-2
; Sequence 2, Application US/09861270
; Patent No. US20020052474A1
; GENERAL INFORMATION:
; APPLICANT: Sul, Hong-Bing
; Goeddel, David V.

; TITLE OF INVENTION: Regulators of Apoptosis
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESS: Science & Technology Law Group
; STREET: 75 Denise Drive
; CITY: Hillsborough
; STATE: California
; COUNTRY: USA
; ZIP: 94010
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/861,270
; FILING DATE: 18-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/795,088
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Ogman, Richard A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 343-4341
; TELEFAX: (650) 343-4342
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 480 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-861-270-2

Query Match 90.8%; Score 1635; DB 9; Length 480;
Best Local Similarity 94.1%; Pred. No. 7.5e-145;
Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;

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DB 97 MAEIGEDLDKSDVSSLIPLMKDYMGRGKISKSEKSFLLDLVVELEKLNVLVAPDQDLDLEKCL 156
QY 61 KNIHRIDLTKIKQYKQSQVQAGTSYRNVLQAAIOKSLKDPNNFR----- 106
DB 157 KNIHRIDLTKIKQYKQSQVQAGTSYRNVLQAAIOKSLKDPNNFRFLHNGRKEQRLKEQ 216
QY 107 ----BEPVKKSIOESEAFIPQSIPEERYKMSKPLGICLIIDICINETELLRTDFTSLGY 162
DB 217 LGAQQEPVKKSIOESEAFIPQSIPEERYKMSKPLGICLIIDICINETELLRTDFTSLGY 276
QY 163 EVQKFLHLSMHGISOILGQFACMPHEHRDYSFVCLVSRGGSQSVYGVVDQTHSGPLHHI 222
DB 277 EVQKFLHLSMHGISOILGQFACMPHEHRDYSFVCLVSRGGSQSVYGVVDQTHSGPLHHI 336
QY 223 RMFMGDCSPYLAKGPKMFFIQQNYVSDGQLESDSSLEVDGPAKKNVEFKAQKRGCTVH 282
DB 337 RMFMGDCSPYLAKGPKMFFIQQNYVSDGQLESDSSLEVDGPAKKNVEFKAQKRGCTVH 396
QY 283 READFFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQER 321
DB 397 READFFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQER 435

RESULT 6
US-09-410-194-11
; Sequence 11, Application US/09410194
; Patent No. US20020095030A1
; GENERAL INFORMATION:
; APPLICANT: Tschoopp, Jurg

```
; APPLICANT: Thome, Margot
; APPLICANT: Burns, Kimberly
; APPLICANT: Immler, Marten
; APPLICANT: Habne, Michael
; APPLICANT: Schroter, Michael
; APPLICANT: Schneider, Pascal
; APPLICANT: Bodmer, Jean- Luc
; APPLICANT: Steiner, Veronique
; APPLICANT: Rimoldi, Donata
; APPLICANT: Hofmann, Kay
; APPLICANT: French, E. Lars
; TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
; FILE REFERENCE: 11141-002001
; CURRENT APPLICATION NUMBER: US/09/410,194
; CURRENT FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: PCT/EP98/01857
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-410-194-11

Query Match          90.8%; Score 1635; DB 9; Length 480;
Best Local Similarity 94.1%; Pred. No. 7.5e-145;
Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;

Qy 1 MAEIGEDLDKSDVSSLIIFLMKDYMGGRGKISKESFLDLVVELEKLNVLAPDQDLDLEKCL 60
Db 97 MAEIGEDLDKSDVSSLIIFLMKDYMGGRGKISKESFLDLVVELEKLNVLAPDQDLDLEKCL 156
Qy 61 KNIHRIDLTKTKYKQSVQAGTSYRNVLQAAIQKSLKDPNNPR----- 106
Db 157 KNIHRIDLTKTKYKQSVQAGTSYRNVLQAAIQKSLKDPNNPRFLHNGRSKEQRLKEQ 216
Qy 107 ----EPPVKKSTQESAEFLPQSIPEERYKMKSKPGICLIIDICINETELLRDITSLGY 162
Db 217 LGAQQEPVKKSTQESAEFLPQSIPEERYKMKSKPGICLIIDICINETELLRDITSLGY 276
Qy 163 EVQKFLHLSMHGISQILGQFACMPHRDYDSFVCVLVSRGSGSQSVYGVVDQTHSGPLPHHI 222
Db 277 EVQKFLHLSMHGISQILGQFACMPHRDYDSFVCVLVSRGSGSQSVYGVVDQTHSGPLPHHI 336
Qy 223 RRMFMGDCPCYLAGPKMFFIQQYVYVSDGQLEDSSLLLEVDPGAMKNVBFKAQKRGICTVH 282
Db 337 RRMFMGDCPCYLAGPKMFFIQQYVYVSDGQLEDSSLLLEVDPGAMKNVBFKAQKRGICTVH 396
Qy 283 READFWSLCTADMSLLEQSHSSPSLYLOCLSQKLRQER 321
Db 397 READFWSLCTADMSLLEQSHSSPSLYLOCLSQKLRQER 435

RESULT 7
US-09-410-194-17
; Sequence 17, Application US/09410194
; Patent No. US20020095030A1
; GENERAL INFORMATION:
; APPLICANT: Thome, Margot
; APPLICANT: Burns, Kimberly
; APPLICANT: Immler, Marten
; APPLICANT: Hahne, Michael
; APPLICANT: Schroter, Michael
; APPLICANT: Schneider, Pascal
; APPLICANT: Bodmer, Jean- Luc
; APPLICANT: Steiner, Veronique
; APPLICANT: Rimoldi, Donata
; APPLICANT: Hofmann, Kay
; APPLICANT: French, E. Lars
```

```
; TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
; FILE REFERENCE: 11141-002001
; CURRENT APPLICATION NUMBER: US/09/410,194
; CURRENT FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: PCT/EP98/01857
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-410-194-17

Query Match          90.8%; Score 1635; DB 9; Length 480;
Best Local Similarity 94.1%; Pred. No. 7.5e-145;
Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;

Qy 1 MAEIGEDLDKSDVSSLIIFLMKDYMGGRGKISKESFLDLVVELEKLNVLAPDQDLDLEKCL 60
Db 97 MAEIGEDLDKSDVSSLIIFLMKDYMGGRGKISKESFLDLVVELEKLNVLAPDQDLDLEKCL 156
Qy 61 KNIHRIDLTKTKYKQSVQAGTSYRNVLQAAIQKSLKDPNNPR----- 106
Db 157 KNIHRIDLTKTKYKQSVQAGTSYRNVLQAAIQKSLKDPNNPRFLHNGRSKEQRLKEQ 216
Qy 107 ----EPPVKKSTQESAEFLPQSIPEERYKMKSKPGICLIIDICINETELLRDITSLGY 162
Db 217 LGAQQEPVKKSTQESAEFLPQSIPEERYKMKSKPGICLIIDICINETELLRDITSLGY 276
Qy 163 EVQKFLHLSMHGISQILGQFACMPHRDYDSFVCVLVSRGSGSQSVYGVVDQTHSGPLPHHI 222
Db 277 EVQKFLHLSMHGISQILGQFACMPHRDYDSFVCVLVSRGSGSQSVYGVVDQTHSGPLPHHI 336
Qy 223 RRMFMGDCPCYLAGPKMFFIQQYVYVSDGQLEDSSLLLEVDPGAMKNVBFKAQKRGICTVH 282
Db 337 RRMFMGDCPCYLAGPKMFFIQQYVYVSDGQLEDSSLLLEVDPGAMKNVBFKAQKRGICTVH 396
Qy 283 READFWSLCTADMSLLEQSHSSPSLYLOCLSQKLRQER 321
Db 397 READFWSLCTADMSLLEQSHSSPSLYLOCLSQKLRQER 435

RESULT 8
US-09-009-893-2
; Sequence 2, Application US/09009893
; Publication No. US20030087339A1
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: ROSEN, CRAIG A.
; APPLICANT: DIXIT, VISHVA M.
; APPLICANT: GENTZ, REINER L.
; APPLICANT: KENNY, JOSEPH J.
; TITLE OF INVENTION: I-FLICE, A NOVEL INHIBITOR OF TUMOR
; TITLE OF INVENTION: NECROSIS FACTOR RECEPTOR-1 AND CD-95 INDUCED APOPTOSIS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: US
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/009,893
; FILING DATE: HERewith
```

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CLASSIFICATION:
PRIOR APPLICATION DATA: US 60/034,205
FILING DATE: 21-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/054,800
FILING DATE: 05-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0970002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 480 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-009-893-2

Query Match          90.8%; Score 1635; DB 10; Length 480;
Best Local Similarity 94.1%; Pred. No. 7.5e-145;
Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;

QY 1 MAEIGEDDKSDVSSLIIFLMKDYMGKISKEKSFLLDLVVELEKLNLVAPDQDLEKCL 60
Db 97 MAEIGEDDKSDVSSLIIFLMKDYMGKISKEKSFLLDLVVELEKLNLVAPDQDLEKCL 156
QY 61 KNIHRIDLTKIQYKQSVQAGTSYRNVLAQAIQKSLKDPNNR----- 106
Db 157 KNIHRIDLTKIQYKQSVQAGTSYRNVLAQAIQKSLKDPNNRFLNHRGSKQRLKEQ 216
QY 107 ----EPPVKYSIQSEAFLPQSIPEERYKMKSKPLGICLIIDICIGNETELLRTFTSLGY 162
Db 217 LQAQEPVKYSIQSEAFLPQSIPEERYKMKSKPLGICLIIDICIGNETELLRTFTSLGY 276
QY 163 EVQKFLHLSMHGISQILGQFACMPHRDYDSFVCLVSRGSGSVYGVVDQTHSGLPLHHI 222
Db 277 EVQKFLHLSMHGISQILGQFACMPHRDYDSFVCLVSRGSGSVYGVVDQTHSGLPLHHI 336
QY 223 RMFMGDCPCYLAGPKMFFIQQYVVSQGLDSSLLVDGPMKNVFEKAKRGGLCTVH 282
Db 337 RMFMGDCPCYLAGPKMFFIQQYVVSQGLDSSLLVDGPMKNVFEKAKRGGLCTVH 396
QY 283 READFFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQER 321
Db 397 READFFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQER 435

RESULT 9
US-09-471-749-1
; Sequence 1, Application US/09471749
; Publication No. US20030124113A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Patterson, Chandra
; APPLICANT: Baughn, Mariah
; TITLE OF INVENTION: HUMAN APOPTOSIS ASSOCIATED PROTEINS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
```

```
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/471,749
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/078,402
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Cerrone, Michael C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PP-0519 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 480 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: TBP1PLB02
CLONE: 157658
US-09-471-749-1

Query Match          90.8%; Score 1635; DB 10; Length 480;
Best Local Similarity 94.1%; Pred. No. 7.5e-145;
Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;

QY 1 MAEIGEDDKSDVSSLIIFLMKDYMGKISKEKSFLLDLVVELEKLNLVAPDQDLEKCL 60
Db 97 MAEIGEDDKSDVSSLIIFLMKDYMGKISKEKSFLLDLVVELEKLNLVAPDQDLEKCL 156
QY 61 KNIHRIDLTKIQYKQSVQAGTSYRNVLAQAIQKSLKDPNNR----- 106
Db 157 KNIHRIDLTKIQYKQSVQAGTSYRNVLAQAIQKSLKDPNNRFLNHRGSKQRLKEQ 216
QY 107 ----EPPVKYSIQSEAFLPQSIPEERYKMKSKPLGICLIIDICIGNETELLRTFTSLGY 162
Db 217 LQAQEPVKYSIQSEAFLPQSIPEERYKMKSKPLGICLIIDICIGNETELLRTFTSLGY 276
QY 163 EVQKFLHLSMHGISQILGQFACMPHRDYDSFVCLVSRGSGSVYGVVDQTHSGLPLHHI 222
Db 277 EVQKFLHLSMHGISQILGQFACMPHRDYDSFVCLVSRGSGSVYGVVDQTHSGLPLHHI 336
QY 223 RMFMGDCPCYLAGPKMFFIQQYVVSQGLDSSLLVDGPMKNVFEKAKRGGLCTVH 282
Db 337 RMFMGDCPCYLAGPKMFFIQQYVVSQGLDSSLLVDGPMKNVFEKAKRGGLCTVH 396
QY 283 READFFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQER 321
Db 397 READFFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQER 435

RESULT 10
US-10-713-208-2
; Sequence 2, Application US/10713208
; Publication No. US20040121387A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: I-FLICE, A Novel Inhibitor of Tumor Necrosis Factor Receptor-1 and
; FILE REFERENCE: CD-95 Induced Apoptosis
; FILE REFERENCE: PF381C1D1
; CURRENT APPLICATION NUMBER: US/10/713,208
; CURRENT FILING DATE: 2003-11-17
; PRIOR APPLICATION NUMBER: US 09/489,155
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/009,893
; PRIOR FILING DATE: 1998-01-21
; PRIOR APPLICATION NUMBER: US 60/054,800
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/034,205
```



```
; PRIOR FILING DATE: 1997-01-21
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-713-208-2

Query Match
Best Local Similarity 90.8%; Score 1635; DB 16; Length 480;
Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;

QY 1 MAEIGEDLDKSDVSSLIPLMKDYMGRGKISKEKSFDLVVELEKLNLVAPDQDLDLEKCL 60
Db MAEIGEDLDKSDVSSLIPLMKDYMGRGKISKEKSFDLVVELEKLNLVAPDQDLDLEKCL 156
QY 61 KNIHRIDLTKTIQKYKQSVQAGTSYRNVLQAAIQKSLKDPNNFR----- 106
Db KNIHRIDLTKTIQKYKQSVQAGTSYRNVLQAAIQKSLKDPNNFR----- 216
QY 107 ----EPPVKYSIQSEAFLPQSIPEERYKMSKPLIGICLIIDCIGNETELLRTDFTSLGY 162
Db LGAQOEPVKYSIQSEAFLPQSIPEERYKMSKPLIGICLIIDCIGNETELLRTDFTSLGY 276
QY 163 EVQKFLHLSMHGSIQILGQFACMPKPFQNYVSDGQLEDSSLLVEDGPMKNVFEKAKRGGLCTVH 222
Db EVQKFLHLSMHGSIQILGQFACMPKPFQNYVSDGQLEDSSLLVEDGPMKNVFEKAKRGGLCTVH 336
QY 223 RRMFMGDCPYLAGPKMFFIQNYVSDGQLEDSSLLVEDGPMKNVFEKAKRGGLCTVH 282
Db RRMFMGDCPYLAGPKMFFIQNYVSDGQLEDSSLLVEDGPMKNVFEKAKRGGLCTVH 396
QY 283 READFFWSLCTADMSLLSEQSHSSPSLYLQCLSQKLRQER 321
Db READFFWSLCTADMSLLSEQSHSSPSLYLQCLSQKLRQER 435

RESULT 12
US-10-832-218-17
; Sequence 17, Application US/10832218
; Publication No. US20050084876A1
; GENERAL INFORMATION:
; APPLICANT: Tschopp, Jurg
; APPLICANT: Thome, Margot
; APPLICANT: Burns, Kimberly
; APPLICANT: Irmeler, Marten
; APPLICANT: Hahne, Michael
; APPLICANT: Schroter, Michael
; APPLICANT: Schneider, Pascal
; APPLICANT: Bodmer, Jean- Luc
; APPLICANT: Steiner, Veronique
; APPLICANT: Rimoldi, Donata
; APPLICANT: Hofmann, Kay
; APPLICANT: French, E. Lars
; TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
; FILE REFERENCE: 11141-002001
; CURRENT APPLICATION NUMBER: US/10/832,218
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: US/09/410,194
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: PCT/EP98/01857
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-832-218-17

Query Match
Best Local Similarity 90.8%; Score 1635; DB 17; Length 480;
Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;

QY 1 MAEIGEDLDKSDVSSLIPLMKDYMGRGKISKEKSFDLVVELEKLNLVAPDQDLDLEKCL 60
Db MAEIGEDLDKSDVSSLIPLMKDYMGRGKISKEKSFDLVVELEKLNLVAPDQDLDLEKCL 156
QY 61 KNIHRIDLTKTIQKYKQSVQAGTSYRNVLQAAIQKSLKDPNNFR----- 106
Db KNIHRIDLTKTIQKYKQSVQAGTSYRNVLQAAIQKSLKDPNNFR----- 216
QY 107 ----EPPVKYSIQSEAFLPQSIPEERYKMSKPLIGICLIIDCIGNETELLRTDFTSLGY 162
Db LGAQOEPVKYSIQSEAFLPQSIPEERYKMSKPLIGICLIIDCIGNETELLRTDFTSLGY 276
QY 163 EVQKFLHLSMHGSIQILGQFACMPKPFQNYVSDGQLEDSSLLVEDGPMKNVFEKAKRGGLCTVH 222
Db EVQKFLHLSMHGSIQILGQFACMPKPFQNYVSDGQLEDSSLLVEDGPMKNVFEKAKRGGLCTVH 336
QY 223 RRMFMGDCPYLAGPKMFFIQNYVSDGQLEDSSLLVEDGPMKNVFEKAKRGGLCTVH 282
Db RRMFMGDCPYLAGPKMFFIQNYVSDGQLEDSSLLVEDGPMKNVFEKAKRGGLCTVH 396
QY 283 READFFWSLCTADMSLLSEQSHSSPSLYLQCLSQKLRQER 321
Db READFFWSLCTADMSLLSEQSHSSPSLYLQCLSQKLRQER 435

RESULT 11
US-10-832-218-11
; Sequence 11, Application US/10832218
; Publication No. US20050084876A1
; GENERAL INFORMATION:
; APPLICANT: Tschopp, Jurg
; APPLICANT: Thome, Margot
; APPLICANT: Burns, Kimberly
; APPLICANT: Irmeler, Marten
; APPLICANT: Hahne, Michael
; APPLICANT: Schroter, Michael
; APPLICANT: Schneider, Pascal
; APPLICANT: Bodmer, Jean- Luc
; APPLICANT: Steiner, Veronique
; APPLICANT: Rimoldi, Donata
; APPLICANT: Hofmann, Kay
; APPLICANT: French, E. Lars
; TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
; FILE REFERENCE: 11141-002001
; CURRENT APPLICATION NUMBER: US/10/832,218
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: US/09/410,194
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: PCT/EP98/01857
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-832-218-11
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Db 157 KNHRIIDLTKIKYKQSVQAGTSYRNVLQAAIQKSLKDPNNFRLHNGRSKEQRLKEQ 216
QY 107 -----EPVKKSIQSEAFIPQSIPEERYKMKSPKPGICLIIDICIGNETELLRTFTTSLGY 162
Db 217 LGAQOEPVKKSIQSEAFIPQSIPEERYKMKSPKPGICLIIDICIGNETELLRTFTTSLGY 276
QY 163 EVQKFLHLSMHGISOILGQFACMPHRDYDSFVCLVLSRGGSSVYGVDTHTSGLPLHHI 222
Db 277 EVQKFLHLSMHGISOILGQFACMPHRDYDSFVCLVLSRGGSSVYGVDTHTSGLPLHHI 336
QY 223 RRMFMGDSCPYLAGKPKMFFIQNYVVSQGLEDSLSLLEVDGPKMKVFEKAKRGKGLCTVH 282
Db 337 RRMFMGDSCPYLAGKPKMFFIQNYVVSQGLEDSLSLLEVDGPKMKVFEKAKRGKGLCTVH 396
QY 283 READPFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQER 321
Db 397 READPFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQER 435

RESULT 13

US-09-764-861-37
; Sequence 37, Application US/09764861
; Publication No. US20020086811A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT204
; CURRENT APPLICATION NUMBER: US/09/764,861
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: SITE
; LOCATION: (97)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-861-37

Query Match 90.6%; Score 1630; DB 9; Length 391;
Best Local Similarity 93.8%; Pred. No. 1.6e-144;
Matches 318; Conservative 2; Mismatches 1; Indels 18; Gaps 1;

QY 1 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKESKSFLLDLVVELEKLNVLAPDQDLLEKCL 60
Db 8 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKESKSFLLDLVVELEKLNVLAPDQDLLEKCL 67
QY 61 KNHRIIDLTKIKYKQSVQAGTSYRNVLQAAIQKSLKDPNNF----- 106
Db 68 KNHRIIDLTKIKYKQSVQAGTSYRNVLQAAIQKSLKDPNNFRLHNGRSKEQRLKEQ 127
QY 107 -----EPVKKSIQSEAFIPQSIPEERYKMKSPKPGICLIIDICIGNETELLRTFTTSLGY 162
Db 128 LGAQOEPVKKSIQSEAFIPQSIPEERYKMKSPKPGICLIIDICIGNETELLRTFTTSLGY 187
QY 163 EVQKFLHLSMHGISOILGQFACMPHRDYDSFVCLVLSRGGSSVYGVDTHTSGLPLHHI 222
Db 188 EVQKFLHLSMHGISOILGQFACMPHRDYDSFVCLVLSRGGSSVYGVDTHTSGLPLHHI 247
QY 223 RRMFMGDSCPYLAGKPKMFFIQNYVVSQGLEDSLSLLEVDGPKMKVFEKAKRGKGLCTVH 282
Db 248 RRMFMGDSCPYLAGKPKMFFIQNYVVSQGLEDSLSLLEVDGPKMKVFEKAKRGKGLCTVH 307
QY 283 READPFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQER 321
Db 308 READPFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQER 346

RESULT 14

US-10-103-313-318
; Sequence 318, Application US/10103313
; Publication No. US20030082758A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJ207C1
; CURRENT APPLICATION NUMBER: US/10/103,313
; CURRENT FILING DATE: 2002-03-12
; NUMBER OF SEQ ID NOS: 653
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 318
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: (97)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-103-313-318

US-09-764-861-37
; Sequence 37, Application US/09764861
; Publication No. US20030171252A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT204
; CURRENT APPLICATION NUMBER: US/09/764,861
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: SITE
; LOCATION: (97)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-861-37

Query Match 90.6%; Score 1630; DB 10; Length 391;
Best Local Similarity 93.8%; Pred. No. 1.6e-144;
Matches 318; Conservative 2; Mismatches 1; Indels 18; Gaps 1;

QY 1 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKESKSFLLDLVVELEKLNVLAPDQDLLEKCL 60
Db 8 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKESKSFLLDLVVELEKLNVLAPDQDLLEKCL 67
QY 61 KNHRIIDLTKIKYKQSVQAGTSYRNVLQAAIQKSLKDPNNF----- 106
Db 68 KNHRIIDLTKIKYKQSVQAGTSYRNVLQAAIQKSLKDPNNFRLHNGRSKEQRLKEQ 127
QY 107 -----EPVKKSIQSEAFIPQSIPEERYKMKSPKPGICLIIDICIGNETELLRTFTTSLGY 162
Db 128 LGAQOEPVKKSIQSEAFIPQSIPEERYKMKSPKPGICLIIDICIGNETELLRTFTTSLGY 187
QY 163 EVQKFLHLSMHGISOILGQFACMPHRDYDSFVCLVLSRGGSSVYGVDTHTSGLPLHHI 222
Db 188 EVQKFLHLSMHGISOILGQFACMPHRDYDSFVCLVLSRGGSSVYGVDTHTSGLPLHHI 247
QY 223 RRMFMGDSCPYLAGKPKMFFIQNYVVSQGLEDSLSLLEVDGPKMKVFEKAKRGKGLCTVH 282
Db 248 RRMFMGDSCPYLAGKPKMFFIQNYVVSQGLEDSLSLLEVDGPKMKVFEKAKRGKGLCTVH 307
QY 283 READPFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQER 321
Db 308 READPFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQER 346

RESULT 15

US-10-103-313-318
; Sequence 318, Application US/10103313
; Publication No. US20030082758A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJ207C1
; CURRENT APPLICATION NUMBER: US/10/103,313
; CURRENT FILING DATE: 2002-03-12
; NUMBER OF SEQ ID NOS: 653
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 318
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: (97)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-103-313-318

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Query Match      90.6%; Score 1630; DB 14; Length 391;
Best Local Similarity 93.8%; Pred.No.1.6e-144;
Matches 318; Conservative 2; Mismatches 1; Indels 18; Gaps 1;

QY 1 MAEIGEDLDKSDVSSLIIFLMKDYMGKGIKSKSFLDLVVELEKLNLVAPDQDLLEKCL 60
Db 8 MAEIGEDLDKSDVSSLIIFLMKDYMGKGIKSKSFLDLVVELEKLNLVAPDQDLLEKCL 67
QY 61 KNHRIIDLTKIKYKQSVQGAGTSYRNVLQAAIQKSLADPSNNPR----- 106
Db 68 KNHRIIDLTKIKYKQSVQGAGTSYRNVLQAAIQKSLADPSNNFLHNGRSKEQRLKEQ 127
QY 107 ----EEPVKKSIQSEAFIPQSIPEERYKMKSKPLGICLIIDCIGNETELLRTFTSLGY 162
Db 128 LGAQQEPVKKSIQSEAFIPQSIPEERYKMKSKPLGICLIIDCIGNETELLRTFTSLGY 187
QY 163 EVQKFLHLSMHGISQILGQFACMPHEHRDYDSFVCLVSRGGSQSVYGVDTHTSGLPPLHHI 222
Db 188 EVQKFLHLSMHGISQILGQFACMPHEHRDYDSFVCLVSRGGSQSVYGVDTHTSGLPPLHHI 247
QY 223 RRMFMGDCPYLAGKPKMFFIQNYVVSQGLSDSSILEVDGPAMKNVEFKAQKRGICTVH 282
Db 248 RRMFMGDCPYLAGKPKMFFIQNYVVSQGLSDSSILEVDGPAMKNVEFKAQKRGICTVH 307
QY 283 READFFWSLCTADMSLLEQSHSSPSLYLQCLSQKLQER 321
Db 308 READFFWSLCTADMSLLEQSHSSPSLYLQCLSQKLQER 346
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Search completed: June 20, 2005, 13:17:59
Job time : 164 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2005, 12:53:13 ; Search time 43 Seconds
(without alignments)
604.137 Million cell updates/sec

Title: US-10-713-208-6
Perfect score: 1800
Sequence: 1 MAEIGEDLDKSDVSSSLIFLM.....ITSEKDMHFSSLGICILLDVL 348

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/1/1aa/PCITUS_COMB.pep:*
6: /cgn2_6/prodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1800	100.0	348	US-09-009-893A-6	Sequence 6, Appli
2	1800	100.0	348	US-09-489-155-6	Sequence 6, Appli
3	1635	90.8	480	US-08-795-088A-2	Sequence 2, Appli
4	1635	90.8	480	US-09-009-893A-2	Sequence 2, Appli
5	1635	90.8	480	US-09-489-155-2	Sequence 2, Appli
6	1579	87.7	480	US-09-069-023-34	Sequence 34, Appli
7	1554.5	86.4	445	US-08-859-167-2	Sequence 2, Appli
8	1554.5	86.4	445	US-09-109-273-2	Sequence 2, Appli
9	1554.5	86.4	445	US-09-276-993-2	Sequence 2, Appli
10	1554.5	86.4	445	US-09-723-450-2	Sequence 2, Appli
11	1270	70.6	244	US-09-949-016-11405	Sequence 11405, A
12	527	29.3	221	US-09-382-155-17	Sequence 17, Appli
13	527	29.3	221	US-09-074-044A-17	Sequence 17, Appli
14	383	21.3	84	US-09-074-044A-2	Sequence 2, Appli
15	369	20.5	84	US-09-382-155-2	Sequence 2, Appli
16	313	17.4	479	US-08-983-502-7	Sequence 7, Appli
17	313	17.4	479	US-09-516-747-7	Sequence 7, Appli
18	313	17.4	479	US-08-851-873-101	Sequence 101, App
19	313	17.4	479	US-09-10521-18	Sequence 18, Appli
20	311.5	17.3	478	US-09-009-893A-3	Sequence 3, Appli
21	311.5	17.3	478	US-09-489-155-3	Sequence 3, Appli
22	311	17.3	479	US-08-807-200-12	Sequence 12, Appli
23	311	17.3	479	US-09-382-155-28	Sequence 28, Appli
24	311	17.3	479	US-09-001-777-12	Sequence 12, Appli
25	311	17.3	479	US-09-074-044A-26	Sequence 26, Appli
26	311	17.3	479	US-09-074-044A-27	Sequence 27, Appli
27	311	17.3	479	US-09-074-044A-28	Sequence 28, Appli

28	309	17.2	479	3	US-08-852-782-3	Sequence 3, Appli
29	306	17.0	479	3	US-09-382-155-27	Sequence 27, Appli
30	304.5	16.9	464	3	US-08-983-502-18	Sequence 18, Appli
31	304.5	16.9	464	4	US-09-516-747-18	Sequence 18, Appli
32	304.5	16.9	464	5	PCT-US96-10521-18	Sequence 18, Appli
33	304.5	16.9	505	4	US-09-949-016-11473	Sequence 11473, A
34	303	16.8	479	3	US-09-382-155-26	Sequence 26, Appli
35	302.5	16.8	389	2	US-08-618-408B-4	Sequence 4, Appli
36	302.5	16.8	496	1	US-08-663-220-4	Sequence 4, Appli
37	302.5	16.8	496	3	US-09-291-692-4	Sequence 4, Appli
38	302.5	16.8	496	4	US-09-952-768-4	Sequence 4, Appli
39	296.5	16.5	476	3	US-09-561-756-27	Sequence 27, Appli
40	296.5	16.5	476	3	US-09-227-721-27	Sequence 27, Appli
41	296.5	16.5	476	4	US-09-954-697-27	Sequence 27, Appli
42	261.5	14.5	335	3	US-08-983-502-16	Sequence 16, Appli
43	261.5	14.5	335	4	US-09-516-747-16	Sequence 16, Appli
44	261.5	14.5	335	5	PCT-US96-10521-16	Sequence 16, Appli
45	248.5	13.8	521	4	US-09-962-834A-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-09-009-893A-6
; Sequence 6, Application US/09009893A

; Patent No. 6623938
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A.
; APPLICANT: Dixit, Vishva M.
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Kenny, Joseph J.
; TITLE OF INVENTION: I-FLICE, A No. 6623938el Inhibitor of Tumor Necrosis Factor Receptor

; FILE REFERENCE: 1488.0970002
; CURRENT APPLICATION NUMBER: US/09/009,893A
; CURRENT FILING DATE: 1998-02-21

; PRIOR APPLICATION NUMBER: US 60/054,800
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/034,205
; PRIOR FILING DATE: 1997-01-21

; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 6
; LENGTH: 348

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-009-893A-6

Query Match 100.0%; Score 1800; DB 4; Length 348;
Best Local Similarity 100.0%; Pred. No. 1.7e-183;
Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MAEIGEDLDKSDVSSSLIFLMKDYMGKISKEKSFLLDLVVELEKLNVAPODLDLEKCL	60
DB	1	MAEIGEDLDKSDVSSSLIFLMKDYMGKISKEKSFLLDLVVELEKLNVAPODLDLEKCL	60
QY	61	KNIHRIIDLTKTKQYKQSVQAGTSYRNVLQAAIQKSLKDPNNFEEPVKKSIQSEAF	120
DB	61	KNIHRIIDLTKTKQYKQSVQAGTSYRNVLQAAIQKSLKDPNNFEEPVKKSIQSEAF	120
QY	121	LPQSIPERYKMKSKPLGICLIIDICIGNETELLRTFTSLGYEVQKFLHLSMHGISOILG	180
DB	121	LPQSIPERYKMKSKPLGICLIIDICIGNETELLRTFTSLGYEVQKFLHLSMHGISOILG	180
QY	181	QFACMPEHRDYDSFVCLVLSRGSSVYGVDDTHSGSLPLHHIRRMFMGDCPCYLAKPKM	240
DB	181	QFACMPEHRDYDSFVCLVLSRGSSVYGVDDTHSGSLPLHHIRRMFMGDCPCYLAKPKM	240
QY	241	FFIQNVVSDGOLEDSSLLLEVDGPAKKNVEFKAQKRGCLCTVHREADFFWSLCTADMSLLE	300
DB	241	FFIQNVVSDGOLEDSSLLLEVDGPAKKNVEFKAQKRGCLCTVHREADFFWSLCTADMSLLE	300

QY 301 QSHSSPSLYLQCLSQKLRQERTIPGSGITKSKMHFSSLGICILLDVL 348
Db 301 QSHSSPSLYLQCLSQKLRQERTIPGSGITKSKMHFSSLGICILLDVL 348

RESULT 2
US-09-489-155-6
; Sequence 6, Application US/09489155
; Patent No. 6680171
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A.
; APPLICANT: Dixit, Vishva M.
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Kenny, Joseph J.
; TITLE OF INVENTION: I-FLICE, A No. 6680171el Inhibitor of Tumor Necrosis Factor Recept
; FILE REFERENCE: CD-95 Induced Apoptosis
; CURRENT APPLICATION NUMBER: US/09/489,155
; CURRENT FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/009,893
; PRIOR FILING DATE: 1998-01-21
; PRIOR APPLICATION NUMBER: US 60/034,205
; PRIOR FILING DATE: 1997-01-21
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 348
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-489-155-6

Query Match 100.0%; Score 1800; DB 4; Length 348;
Best Local Similarity 100.0%; Pred. No. 1.7e-183; Indels 0; Gaps 0;
Matches 348; Conservative 0; Mismatches 0;

QY 1 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKESFLDLVVELEKLNVLVAPDQDLLEKCL 60
Db 1 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKESFLDLVVELEKLNVLVAPDQDLLEKCL 60

QY 61 KNIHRIDLTKTKYKQSVQAGTSYRNVLQAAIQKSLKDPNNFRLHNGRSKEQRLKEQ 120
Db 61 KNIHRIDLTKTKYKQSVQAGTSYRNVLQAAIQKSLKDPNNFRLHNGRSKEQRLKEQ 120

QY 121 LPQSIPEERYKMKSKPLGICLIIDICIGNETELLRTFTSLGYEVQKFLHLSMHGISOILG 180
Db 121 LPQSIPEERYKMKSKPLGICLIIDICIGNETELLRTFTSLGYEVQKFLHLSMHGISOILG 180

QY 181 QFACMPEHRDYSFVCLVSRGSSQSVYGVQDTHSGPLPLHHIRRMFMGSDSCPYLAGKPKM 240
Db 181 QFACMPEHRDYSFVCLVSRGSSQSVYGVQDTHSGPLPLHHIRRMFMGSDSCPYLAGKPKM 240

QY 241 FFIQNVVSDGQLEDSSLLLEVDPAMKNVEFKAQKRGICLVHREADFFWLSLCTADMSLLE 300
Db 241 FFIQNVVSDGQLEDSSLLLEVDPAMKNVEFKAQKRGICLVHREADFFWLSLCTADMSLLE 300

QY 301 QSHSSPSLYLQCLSQKLRQERTIPGSGITKSKMHFSSLGICILLDVL 348
Db 301 QSHSSPSLYLQCLSQKLRQERTIPGSGITKSKMHFSSLGICILLDVL 348

RESULT 3
US-08-795-088A-2
; Sequence 2, Application US/08795088A
; Patent No. 6242569
; GENERAL INFORMATION:
; APPLICANT: Sul, Hong-Bing
; APPLICANT: Goeddel, David V.
; TITLE OF INVENTION: Regulators of Apoptosis
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Science & Technology Law Group

STREET: 75 Denise Drive
CITY: Hillsborough
STATE: California
COUNTRY: USA
ZIP: 94010
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,088A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 480 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-795-088A-2

Query Match 90.8%; Score 1635; DB 3; Length 480;
Best Local Similarity 94.1%; Pred. No. 1.2e-165;
Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;

QY 1 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKESFLDLVVELEKLNVLVAPDQDLLEKCL 60
Db 97 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKESFLDLVVELEKLNVLVAPDQDLLEKCL 156

QY 61 KNIHRIDLTKTKYKQSVQAGTSYRNVLQAAIQKSLKDPNNFRLHNGRSKEQRLKEQ 106
Db 157 KNIHRIDLTKTKYKQSVQAGTSYRNVLQAAIQKSLKDPNNFRLHNGRSKEQRLKEQ 216

QY 107 ----REPVKYSIQSEAFLPQSIPEERYKMKSKPLGICLIIDICIGNETELLRTFTSLGY 162
Db 217 LGAQQEPVKYSIQSEAFLPQSIPEERYKMKSKPLGICLIIDICIGNETELLRTFTSLGY 276

QY 163 EVQKFLHLSMHGISOILGQFACMPEHRDYSFVCLVSRGSSQSVYGVQDTHSGPLPLHHI 222
Db 277 EVQKFLHLSMHGISOILGQFACMPEHRDYSFVCLVSRGSSQSVYGVQDTHSGPLPLHHI 336

QY 223 RRMFMGSDSCPYLAGKPKMFFIQNVVSDGQLEDSSLLLEVDPAMKNVEFKAQKRGICLVH 282
Db 337 RRMFMGSDSCPYLAGKPKMFFIQNVVSDGQLEDSSLLLEVDPAMKNVEFKAQKRGICLVH 396

QY 283 READFFWLSLCTADMSLLEQSHSSPSLYLQCLSQKLRQER 321
Db 397 READFFWLSLCTADMSLLEQSHSSPSLYLQCLSQKLRQER 435

RESULT 4
US-09-009-893A-2
; Sequence 2, Application US/09009893A
; Patent No. 6623938
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A.
; APPLICANT: Dixit, Vishva M.
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Kenny, Joseph J.
; TITLE OF INVENTION: I-FLICE, A No. 6623938el Inhibitor of Tumor Necrosis Factor Recept
; FILE REFERENCE: CD-95 Induced Apoptosis
; CURRENT APPLICATION NUMBER: US/09/009,893A

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; CURRENT FILING DATE: 1998-02-21
; PRIOR APPLICATION NUMBER: US 60/054,800
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/034,205
; PRIOR FILING DATE: 1997-01-21
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 2
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-009-893A-2

Query Match
Best Local Similarity 90.8%; Score 1635; DB 4; Length 480;
Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;

QY 1 MAEIGEDLDKSDVSSLIIFLMKDYMGKGKISKESFLDLVVELEKLNVLAPDQDLDLEKCL 60
DB 97 MAEIGEDLDKSDVSSLIIFLMKDYMGKGKISKESFLDLVVELEKLNVLAPDQDLDLEKCL 156

QY 61 KNIHRIDLTKTKIQKYKQSVQAGTGYRNVLQAAIQKSLKDPNNFR----- 106
DB 157 KNIHRIDLTKTKIQKYKQSVQAGTGYRNVLQAAIQKSLKDPNNFR----- 216

QY 107 ----BEPVKKSTQSEAFIPQSIPEERYKMKSKPLGICLIIDICIGNETELLRTDTFTSLGY 162
DB 217 LGAQQEPVKKSTQSEAFIPQSIPEERYKMKSKPLGICLIIDICIGNETELLRTDTFTSLGY 276

QY 163 EVQKFLHLSMHGISOILGQFACMPHERDYDFVCLVSRGSGSVYGVDTHTSGLPLHHI 222
DB 277 EVQKFLHLSMHGISOILGQFACMPHERDYDFVCLVSRGSGSVYGVDTHTSGLPLHHI 336

QY 223 RMFMGDCSPYLAGPKMFFIQNYVYVSDQLEDSSLELVDGPMKKNVEFKAQKRGCLCTVH 282
DB 337 RMFMGDCSPYLAGPKMFFIQNYVYVSDQLEDSSLELVDGPMKKNVEFKAQKRGCLCTVH 396

QY 283 READPFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQER 321
DB 397 READPFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQER 435

RESULT 6
US-09-069-023-34
; Sequence 34, Application US/09069023A
; Patent No. 6348573
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; APPLICANT: Koseki, Takeyoshi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
; FILE REFERENCE: UM-0333
; CURRENT APPLICATION NUMBER: US/09/069,023A
; CURRENT FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 34
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-069-023-34

Query Match
Best Local Similarity 87.7%; Score 1579; DB 3; Length 480;
Matches 309; Conservative 4; Mismatches 8; Indels 18; Gaps 1;

QY 1 MAEIGEDLDKSDVSSLIIFLMKDYMGKGKISKESFLDLVVELEKLNVLAPDQDLDLEKCL 60
DB 97 MAEIGEDLDKSDVSSLIIFLMKDYMGKGKISKESFLDLVVELEKLNVLAPDQDLDLEKCL 156

QY 61 KNIHRIDLTKTKIQKYKQSVQAGTGYRNVLQAAIQKSLKDPNNFR----- 106
DB 157 KNIHRIDLTKTKIQKYKQSVQAGTGYRNVLQAAIQKSLKDPNNFR----- 216

QY 107 ----BEPVKKSTQSEAFIPQSIPEERYKMKSKPLGICLIIDICIGNETELLRTDTFTSLGY 162
DB 217 LGAQQEPVKKSTQSEAFIPQSIPEERYKMKSKPLGICLIIDICIGNETELLRTDTFTSLGY 276

QY 163 EVQKFLHLSMHGISOILGQFACMPHERDYDFVCLVSRGSGSVYGVDTHTSGLPLHHI 222
DB 277 EVQKFLHLSMHGISOILGQFACMPHERDYDFVCLVSRGSGSVYGVDTHTSGLPLHHI 336

QY 223 RMFMGDCSPYLAGPKMFFIQNYVYVSDQLEDSSLELVDGPMKKNVEFKAQKRGCLCTVH 282
DB 337 RMFMGDCSPYLAGPKMFFIQNYVYVSDQLEDSSLELVDGPMKKNVEFKAQKRGCLCTVH 396

QY 283 READPFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQER 321
DB 397 READPFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQER 435

; CURRENT FILING DATE: 1998-02-21
; PRIOR APPLICATION NUMBER: US 60/054,800
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/034,205
; PRIOR FILING DATE: 1997-01-21
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 2
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-009-893A-2

Query Match
Best Local Similarity 90.8%; Score 1635; DB 4; Length 480;
Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;

QY 1 MAEIGEDLDKSDVSSLIIFLMKDYMGKGKISKESFLDLVVELEKLNVLAPDQDLDLEKCL 60
DB 97 MAEIGEDLDKSDVSSLIIFLMKDYMGKGKISKESFLDLVVELEKLNVLAPDQDLDLEKCL 156

QY 61 KNIHRIDLTKTKIQKYKQSVQAGTGYRNVLQAAIQKSLKDPNNFR----- 106
DB 157 KNIHRIDLTKTKIQKYKQSVQAGTGYRNVLQAAIQKSLKDPNNFR----- 216

QY 107 ----BEPVKKSTQSEAFIPQSIPEERYKMKSKPLGICLIIDICIGNETELLRTDTFTSLGY 162
DB 217 LGAQQEPVKKSTQSEAFIPQSIPEERYKMKSKPLGICLIIDICIGNETELLRTDTFTSLGY 276

QY 163 EVQKFLHLSMHGISOILGQFACMPHERDYDFVCLVSRGSGSVYGVDTHTSGLPLHHI 222
DB 277 EVQKFLHLSMHGISOILGQFACMPHERDYDFVCLVSRGSGSVYGVDTHTSGLPLHHI 336

QY 223 RMFMGDCSPYLAGPKMFFIQNYVYVSDQLEDSSLELVDGPMKKNVEFKAQKRGCLCTVH 282
DB 337 RMFMGDCSPYLAGPKMFFIQNYVYVSDQLEDSSLELVDGPMKKNVEFKAQKRGCLCTVH 396

QY 283 READPFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQER 321
DB 397 READPFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQER 435

RESULT 5
US-09-489-155-2
; Sequence 2, Application US/09489155
; Patent No. 6680171
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A.
; APPLICANT: Dixit, Vishva M.
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Kenny, Joseph J.
; TITLE OF INVENTION: I-FLICE, A No. 6680171el Inhibitor of Tumor Necrosis Factor Receptor
; TITLE OF INVENTION: CD-95 Induced Apoptosis
; FILE REFERENCE: 1488.0970002
; CURRENT APPLICATION NUMBER: US/09/489,155
; CURRENT FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/009,893
; PRIOR FILING DATE: 1998-01-21
; PRIOR APPLICATION NUMBER: US 60/034,205
; PRIOR FILING DATE: 1997-01-21
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 2
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-489-155-2

Query Match
Best Local Similarity 94.1%; Score 1635; DB 4; Length 480;
Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;
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RESULT 7
US-08-859-167-2
; Sequence 2, Application US/08859167
; Patent No. 6037461
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF
; TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS
; TITLE OF INVENTION: OF MAKING THE SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6037461iris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: WINDOWS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,167
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/859,167
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 445 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-859-167-2

Query Match      86.4%; Score 1554.5; DB 3; Length 445;
Best Local Similarity 94.4%; Pred. No. 4.2e-157;
Matches 303; Conservative 1; Mismatches 0; Indels 17; Gaps 1;

QY 1 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKEKSFDDLVLVELEKLNVLVAPDQDLLEKCL 60
DB 97 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKEKSFDDLVLVELEKLNVLVAPDQDLLEKCL 156
QY 61 KNHRIIDLTKIQKYQSVQAGTSYRNVLQAAIOKSLKDPSPNNFPREEPVKKSIOESEAF 120
DB 157 KNHRIIDLTKIQKYQSVQAGTSYRNVLQAAIOKSLKDPSPNNFR-----202
QY 121 LPQSIPEERYKMKSKPLGICLIIDICIGNETELRLDTFTSLGYEVQKFLHLSMHGISQILG 180
DB 203 ---SIPEERYKMKSKPLGICLIIDICIGNETELRLDTFTSLGYEVQKFLHLSMHGISQILG 259
QY 181 QFACMPHEHRDYSFVCLVLSRGSQSVYGVQDTHSGSLPLHHIRRMFMGSDCPYLACKPKM 240
DB 260 QFACMPHEHRDYSFVCLVLSRGSQSVYGVQDTHSGSLPLHHIRRMFMGSDCPYLACKPKM 319
QY 241 FFIQNTVYVSDGQLEDSSLLLEVDPGAMKNVEFKAQKRGCLCTVHREADFFWSLCTADMSSLE 300
DB 320 FFIQNTVYVSDGQLEDSSLLLEVDPGAMKNVEFKAQKRGCLCTVHREADFFWSLCTADMSSLE 379
QY 301 QSHSSPSLYLQCLISOKLROER 321
DB 380 QSHSSPSLYLQCLISOKLROER 400

RESULT 8
US-09-109-273-2
; Sequence 2, Application US/09109273
; Patent No. 6063760
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF
; TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS
; TITLE OF INVENTION: OF MAKING THE SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6063760iris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: WINDOWS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/109,273
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/859,167
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 445 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-109-273-2

Query Match      86.4%; Score 1554.5; DB 3; Length 445;
Best Local Similarity 94.4%; Pred. No. 4.2e-157;
Matches 303; Conservative 1; Mismatches 0; Indels 17; Gaps 1;

QY 1 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKEKSFDDLVLVELEKLNVLVAPDQDLLEKCL 60
DB 97 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKEKSFDDLVLVELEKLNVLVAPDQDLLEKCL 156
QY 61 KNHRIIDLTKIQKYQSVQAGTSYRNVLQAAIOKSLKDPSPNNFPREEPVKKSIOESEAF 120
DB 157 KNHRIIDLTKIQKYQSVQAGTSYRNVLQAAIOKSLKDPSPNNFR-----202
QY 121 LPQSIPEERYKMKSKPLGICLIIDICIGNETELRLDTFTSLGYEVQKFLHLSMHGISQILG 180
DB 203 ---SIPEERYKMKSKPLGICLIIDICIGNETELRLDTFTSLGYEVQKFLHLSMHGISQILG 259
QY 181 QFACMPHEHRDYSFVCLVLSRGSQSVYGVQDTHSGSLPLHHIRRMFMGSDCPYLACKPKM 240
DB 260 QFACMPHEHRDYSFVCLVLSRGSQSVYGVQDTHSGSLPLHHIRRMFMGSDCPYLACKPKM 319
QY 241 FFIQNTVYVSDGQLEDSSLLLEVDPGAMKNVEFKAQKRGCLCTVHREADFFWSLCTADMSSLE 300
DB 320 FFIQNTVYVSDGQLEDSSLLLEVDPGAMKNVEFKAQKRGCLCTVHREADFFWSLCTADMSSLE 379
QY 301 QSHSSPSLYLQCLISOKLROER 321
DB 380 QSHSSPSLYLQCLISOKLROER 400
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RESULT 9

US-09-276-993-2
; Sequence 2, Application US/09276993
; Patent No. 6207801
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF
; TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS
; TITLE OF INVENTION: OF MAKING THE SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6207801iris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: WINDOWS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/276,993
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/859,167
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 445 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-09-276-993-2

Query Match 86.4%; Score 1554.5; DB 3; Length 445;
Best Local Similarity 94.4%; Pred. No. 4.2e-157;
Matches 303; Conservative 1; Mismatches 0; Indels 17; Gaps 1;

QY 1 MAEIGEDLDKSDVSSLIIFLMKDYMGKGKISKEKSFLLDLVVELEKLNVLAPDQDLLEKCL 60
DB 97 MAEIGEDLDKSDVSSLIIFLMKDYMGKGKISKEKSFLLDLVVELEKLNVLAPDQDLLEKCL 156

QY 61 KNHRIIDLTKTKQYKQSVQAGTSYRNVLQAAIQKSLKDPSPNFPREEPVKSIQSEAF 120
DB 157 KNHRIIDLTKTKQYKQSVQAGTSYRNVLQAAIQKSLKDPSPNFR----- 202

QY 121 LPQSIPEERYKMKSKPLGICLIIDICINETELLRTDFTSLGYEVQKFLHLSMHGISOILG 180
DB 203 ---SIPEERYKMKSKPLGICLIIDICINETELLRTDFTSLGYEVQKFLHLSMHGISOILG 259

QY 181 QFACMPERHDYDSFVCLVSRGSGSVYGVQDTHSGPLPLHHIRRMFMGDSCPYLACKPKM 240
DB 260 QFACMPERHDYDSFVCLVSRGSGSVYGVQDTHSGPLPLHHIRRMFMGDSCPYLACKPKM 319

QY 241 FTQNYVVSDDGLEDSSLLLEVDPKAMKNVEFKAQKRGCLCTVHREADFFWSLCTADMSSLE 300
DB 320 FTQNYVVSDDGLEDSSLLLEVDPKAMKNVEFKAQKRGCLCTVHREADFFWSLCTADMSSLE 379

QY 301 QSHSSPSLYLQCLSQKLRQER 321
DB 380 QSHSSPSLYLQCLSQKLRQER 400

RESULT 11

US-09-949-016-11405
; Sequence 11405, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498

Query Match 86.4%; Score 1554.5; DB 4; Length 445;
Best Local Similarity 94.4%; Pred. No. 4.2e-157;
Matches 303; Conservative 1; Mismatches 0; Indels 17; Gaps 1;

QY 1 MAEIGEDLDKSDVSSLIIFLMKDYMGKGKISKEKSFLLDLVVELEKLNVLAPDQDLLEKCL 60
DB 97 MAEIGEDLDKSDVSSLIIFLMKDYMGKGKISKEKSFLLDLVVELEKLNVLAPDQDLLEKCL 156

QY 61 KNHRIIDLTKTKQYKQSVQAGTSYRNVLQAAIQKSLKDPSPNFPREEPVKSIQSEAF 120
DB 157 KNHRIIDLTKTKQYKQSVQAGTSYRNVLQAAIQKSLKDPSPNFR----- 202

QY 121 LPQSIPEERYKMKSKPLGICLIIDICINETELLRTDFTSLGYEVQKFLHLSMHGISOILG 180
DB 203 ---SIPEERYKMKSKPLGICLIIDICINETELLRTDFTSLGYEVQKFLHLSMHGISOILG 259

QY 181 QFACMPERHDYDSFVCLVSRGSGSVYGVQDTHSGPLPLHHIRRMFMGDSCPYLACKPKM 240
DB 260 QFACMPERHDYDSFVCLVSRGSGSVYGVQDTHSGPLPLHHIRRMFMGDSCPYLACKPKM 319

QY 241 FTQNYVVSDDGLEDSSLLLEVDPKAMKNVEFKAQKRGCLCTVHREADFFWSLCTADMSSLE 300
DB 320 FTQNYVVSDDGLEDSSLLLEVDPKAMKNVEFKAQKRGCLCTVHREADFFWSLCTADMSSLE 379

QY 301 QSHSSPSLYLQCLSQKLRQER 321
DB 380 QSHSSPSLYLQCLSQKLRQER 400


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; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11405
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11405

Query Match          70.6%; Score 1270; DB 4; Length 244;
Best Local Similarity 99.2%; Pred. No. 4e-127; Indels 0; Gaps 0;
Matches 241; Conservative 2; Mismatches 0;

QY 106 REBPVKSIQESAFIPQSIPEERYKMKSPKPLGICILIIDICINETELLRTDTTSLGYEVQ 165
Db 2 QEEPVKSIQESAFIPQSIPEERYKMKSPKPLGICILIIDICINETELLRTDTTSLGYEVQ 61

QY 166 KFLHLSMHGISQILGQFACWPEHRDYDSFVCLVSRGSGSVYGVQDTHSGPLHHIRM 225
Db 62 KFLHLSMHGISQILGQFACWPEHRDYDSFVCLVSRGSGSVYGVQDTHSGPLHHIRM 121

QY 226 FMGDSCPYLAGKPKMFFIYQNVVSDGLEDSSILEVDGPMKNVEPKAKRGICTVHREA 285
Db 122 FMGDSCPYLAGKPKMFFIYQNVVSDGLEDSSILEVDGPMKNVEPKAKRGICTVHREA 181

QY 286 DFFWLSCTADMSLLEQSHSPSLYLQCLSQKLRQERTIPGSGITESKDMHFSGLCILL 345
Db 182 DFFWLSCTADMSLLEQSHSPSLYLQCLSQKLRQERTIPGSGITESKDMHFSGLCILL 241

QY 346 DVL 348
Db 242 DVL 244

RESULT 12
US-09-382-155-17
; Sequence 17, Application US/09382155B
; Patent No. 6160095
; GENERAL INFORMATION:
; APPLICANT: CHAUDHARY, PREET M
; APPLICANT: HOOD, LEROY
; TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NF-kB, JNK AND APOPTOSIS
; FILE OF INVENTION: PATHWAYS AND METHODS OF USING THE SAME
; FILE REFERENCE: Chaudhary
; CURRENT FILING DATE: 1999-08-24
; CURRENT APPLICATION NUMBER: US/09/382,155B
; EARLIER APPLICATION NUMBER: 09/074,044
; EARLIER FILING DATE: 1998-05-07
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-382-155-17

Query Match          29.3%; Score 527; DB 3; Length 221;
Best Local Similarity 100.0%; Pred. No. 7.8e-48; Indels 0; Gaps 0;
Matches 106; Conservative 0; Mismatches 0;

QY 1 MAEIGEDLDKSDVSSLIIFLMKDYMGKGKISKEKSFIDLVLVELEKLNLVAPDQDLLEKCL 60
Db 97 MAEIGEDLDKSDVSSLIIFLMKDYMGKGKISKEKSFIDLVLVELEKLNLVAPDQDLLEKCL 156

QY 61 KNIHRIDLTKTKIQKYQSVQAGTSYRNVLQAAIQSKLKDPSNNFR 106
Db 157 KNIHRIDLTKTKIQKYQSVQAGTSYRNVLQAAIQSKLKDPSNNFR 202

RESULT 13
US-09-074-044A-17
; Sequence 17, Application US/09074044A
; Patent No. 6207458
; GENERAL INFORMATION:
; APPLICANT: CHAUDHARY, PREET M
; APPLICANT: HOOD, LEROY
; TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NF-kB, JNK AND
; FILE OF INVENTION: APOPTOSIS PATHWAYS AND METHODS OF USING THE SAME
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
; STREET: 2405 GRAND BLVD., SUITE 400
; CITY: KANSAS CITY
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; ORGANISM: Homo sapiens
US-09-074-044A-17

Query Match          29.3%; Score 527; DB 3; Length 221;
Best Local Similarity 100.0%; Pred. No. 7.8e-48; Indels 0; Gaps 0;
Matches 106; Conservative 0; Mismatches 0;

QY 1 MAEIGEDLDKSDVSSLIIFLMKDYMGKGKISKEKSFIDLVLVELEKLNLVAPDQDLLEKCL 60
Db 97 MAEIGEDLDKSDVSSLIIFLMKDYMGKGKISKEKSFIDLVLVELEKLNLVAPDQDLLEKCL 156

QY 61 KNIHRIDLTKTKIQKYQSVQAGTSYRNVLQAAIQSKLKDPSNNFR 106
Db 157 KNIHRIDLTKTKIQKYQSVQAGTSYRNVLQAAIQSKLKDPSNNFR 202

RESULT 14
US-09-074-044A-2
; Sequence 2, Application US/09074044A
; Patent No. 6207458
; GENERAL INFORMATION:
; APPLICANT: CHAUDHARY, PREET M
; APPLICANT: HOOD, LEROY
; TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NF-kB, JNK AND
; FILE OF INVENTION: APOPTOSIS PATHWAYS AND METHODS OF USING THE SAME
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
; STREET: 2405 GRAND BLVD., SUITE 400
; CITY: KANSAS CITY
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; ORGANISM: Homo sapiens
US-09-074-044A-17
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/074,044A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COLLINS, JOHN M
REGISTRATION NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 26588
TELECOMMUNICATION INFORMATION:
TELEPHONE: 816/474-9050
TELEFAX: 816/474-9057
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: not relevant
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-09-074-044A-2

Query Match 21.3%; Score 383; DB 3; Length 84;
Best Local Similarity 100.0%; Pred. No. 4e-33;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEIGDLDKSDVSSLIFLMKDYMGRGKISKESFLDLVVELEKLNLVAPDQDLDLEKCL 60
DB 8 MAEIGDLDKSDVSSLIFLMKDYMGRGKISKESFLDLVVELEKLNLVAPDQDLDLEKCL 67

QY 61 KNHRIIDLTKTKIOKYKQ 77
DB 68 KNHRIIDLTKTKIOKYKQ 84

RESULT 15
US-09-382-155-2
Sequence 2, Application US/09382155B
Patent No. 6160095
GENERAL INFORMATION:
APPLICANT: CHAUDHARY, PREET M
APPLICANT: HOOD, LEROY
TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NF-kB, JNK AND APOPTOSIS
TITLE OF INVENTION: PATHWAYS AND METHODS OF USING THE SAME
FILE REFERENCE: Chaudhary
CURRENT APPLICATION NUMBER: US/09/382,155B
CURRENT FILING DATE: 1999-08-24
EARLIER APPLICATION NUMBER: 09/074,044
EARLIER FILING DATE: 1998-05-07
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 84
TYPE: PRT
ORGANISM: HUMAN HERPESVIRUS 8
US-09-382-155-2

Query Match 20.5%; Score 369; DB 3; Length 84;
Best Local Similarity 97.4%; Pred. No. 1.3e-31;
Matches 75; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MAEIGDLDKSDVSSLIFLMKDYMGRGKISKESFLDLVVELEKLNLVAPDQDLDLEKCL 60
DB 8 MAEIGDLDKSDVSSLIFLMKDYMGRGKISKESFLDLVVELEKLNLVAPDQDLDLEKCL 67

QY 61 KNHRIIDLTKTKIOKYKQ 77
DB 68 KNHRIIDLTKTKIOKYKQ 84

Search completed: June 20, 2005, 13:06:55
Job time : 44 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2005, 13:07:04 ; Search time 38 Seconds
(without alignments)
189.902 Million cell updates/sec

Title: US-10-713-208-6_COPY_1_75
Perfect score: 373
Sequence: 1 MAEIGEDLDKSDVSSLIPLM.....LEKCLKNIHRIIDLTKTIQKY 75

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 23404

Minimum DB seq length: 0
Maximum DB seq length: 75

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	15.0	60	2 I39957	degradative enzyme
2	53.5	14.3	59	2 C36493	H+-transporting tw
3	53	14.2	48	2 H83759	hypothetical prote
4	50.5	13.5	66	2 AF3493	hypothetical cytos
5	50.5	13.5	68	2 F69799	hypothetical prote
6	49.5	13.3	70	2 B64497	hypothetical prote
7	48.5	13.0	66	2 G71834	ribosomal protein
8	48.5	13.0	66	2 T00821	hypothetical prote
9	47.5	12.7	62	2 T12832	hypothetical prote
10	47	12.6	40	2 S45688	glutathione transf
11	46	12.3	46	2 C81322	very hypothetical
12	45.5	12.2	44	2 F70275	hypothetical prote
13	45.5	12.2	58	2 D89871	conserved hypothet
14	45.5	12.2	60	2 T12910	hypothetical prote
15	45	12.1	45	2 B43959	ORF overlapping ca
16	45	12.1	40	2 A34945	transcription regu
17	45	12.1	62	2 S77797	phosphopyruvate hy
18	45	12.1	62	2 C90761	probable division
19	45	12.1	62	2 H85624	hypothetical prote
20	45	12.1	72	2 B69705	transcription regu
21	45	12.1	74	2 A10546	hypothetical prote
22	45	12.1	74	2 E84127	hypothetical prote
23	44.5	11.9	66	2 G64883	ribosomal protein
24	44.5	11.9	71	2 T07852	probable DNA-direc
25	44	11.8	66	2 T12638	homeotic protein H
26	44	11.8	71	2 AC2362	30S ribosomal prot
27	44	11.8	73	2 T38402	hypothetical prote
28	43.5	11.7	30	2 S34761	L-serine ammonia-1
29	43.5	11.7	64	2 T39013	hypothetical prote

30	43	11.5	70	2 S77883	hypothetical prote
31	42.5	11.4	65	2 C82339	hypothetical prote
32	42.5	11.4	66	2 C97870	oxidoreductase hom
33	42.5	11.4	74	2 E90827	hypothetical prote
34	42.5	11.4	74	2 C96547	hypothetical prote
35	42	11.3	57	2 C97758	hypothetical prote
36	42	11.3	65	2 T03652	probable carbonate
37	42	11.3	70	2 S48885	DNA-directed RNA p
38	41.5	11.1	65	2 C82290	hypothetical prote
39	41.5	11.1	67	2 H96936	probable metal-bin
40	41.5	11.1	72	2 G72399	ribosomal protein
41	41.5	11.1	73	2 E95078	conserved hypothet
42	41.5	11.1	75	2 AB1245	exodeoxyribonuclea
43	41.5	11.1	75	2 AF1607	exodeoxyribonuclea
44	41	11.0	40	2 T07583	hypothetical prote
45	41	11.0	50	2 H81250	hypothetical prote

ALIGNMENTS

RESULT 1

I39957
degradative enzyme production factor degR - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
C:Accession: I39957; I39958; A69614
R:Nagami, Y.; Tanaka, T.
J. Bacteriol. 166, 20-28, 1986
A:Title: Molecular cloning and nucleotide sequence of a DNA fragment from Bacillus natto
A:Reference number: I39957; MUID:86168015; PMID:3082853
A:Accession: I39957
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-60 <RES>
A:Cross-references: UNIPROT:P06563; GB:M12917; NID:g143354; PIDN:AAA22671.1; PID:g143355
R:Yang, M.; Shimotzu, H.; Ferrari, E.; Henner, D.J.
J. Bacteriol. 169, 434-437, 1987
A:Title: Characterization and mapping of the Bacillus subtilis prtr gene.
A:Reference number: I39958; MUID:87083406; PMID:3098734
A:Accession: I39958
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-60 <RE2>
A:Cross-references: GB:M15318; NID:g143356; PIDN:AAA22672.1; PID:g143357
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertorello, C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi, A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallucci, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Hoisappel, S.; Hosono, S.; Hullo, M.F.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y. M.; Ogawa, K.; Ogihara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serot, akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpsstra, P.; Tognoni, A.; Torato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K. A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: A69614
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-60 <KUN>
A:Cross-references: GB:Z99115; GB:AL009126; NID:g2634478; PIDN:CAB14112.1; PID:e1183641; C:Experimental source: strain 168
C:Genetics:
A:Gene: degR

Query Match 15.0%; Score 56; DB 2; Length 60;
Best Local Similarity 27.8%; Pred. No. 45;
Matches 15; Conservative 14; Mismatches 17; Indels 8; Gaps 1;

A:Reference number: A64300; MUID:96337999; PMID:8688087
A:Accession: B64497
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-70 <BUL>
A:Cross-references: UNIPROT:Q58974; GB:U67598; GB:L77117; NID:g1592196; PIDN:AAB99607.1;
C:Genetics:
A:Map position: REV1555147-1554935

Query Match 13.3%; Score 49.5; DB 2; Length 70;
Best Local Similarity 29.2%; Pred. No. 2.4e+02;
Matches 19; Conservative 12; Mismatches 29; Indels 5; Gaps 2;

QY 10 KSDVSLIFLMKDYMGKISKEKSFLLVVELEKLNIVAPDQLLEKLNHRIIDIK 69
DB 4 RKEIELMFVLPYMANMEFIKE--LLESVNSLEELE--QKVRELEKEITDKTKDLK 58

QY 70 TKIQK 74
DB 59 ILLEK 63

RESULT 7
G71834
ribosomal protein L29 - Helicobacter pylori (strain J99)
C:Species: Helicobacter pylori
A:Variety: strain J99
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C:Accession: G71834
R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
Ive, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A:Reference number: A71800; MUID:99120557; PMID:9923682
A:Accession: G71834
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-66 <ARN>
A:Cross-references: UNIPROT:Q92J81; GB:AE001547; GB:AE001439; NID:g4155811; PIDN:AAD0679
A:Experimental source: strain J99
C:Genetics:
A:Gene: rpmC
C:Superfamily: Escherichia coli ribosomal protein L29

Query Match 13.0%; Score 48.5; DB 2; Length 66;
Best Local Similarity 30.4%; Pred. No. 2.9e+02;
Matches 14; Conservative 12; Mismatches 15; Indels 5; Gaps 2;

QY 30 SKEKSFLLVVELEKLNIVAPDQLLEKLNHRIIDIKTKIQKY 75
DB 20 AKKAELFELRVKLNQNSPNE---IKKARRNIARIN--TAINAY 60

RESULT 8
T00821
hypothetical protein A22941650 [imported] - Arabidopsis thaliana
N:Alternate names: hypothetical protein T32G6.17
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C:Accession: T00821; D84844
R:Rounsley, S.D.; Lin, X.; Kechum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul
submitted to the EMBL Data Library, November 1997
A:Description: Arabidopsis thaliana chromosome II BAC T32G6 genomic sequence.
A:Reference number: Z14163
A:Accession: T00821
A:Status: translated from GB/EMBL/DBSJ
A:Molecule type: DNA
A:Residues: 1-66 <ROU>
A:Cross-references: UNIPROT:O22226; EMBL:AC002510; NID:g2618683; PID:g2618700
A:Experimental source: cultivar Columbia
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.L.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10611797
A:Accession: D84844
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-66 <STO>
A:Cross-references: GB:AE002093; NID:g2618700; PIDN:AAB84347.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g41650; T32G6.17
A:Map position: 2
A:Introns: 5/2

Query Match 13.0%; Score 48.5; DB 2; Length 66;
Best Local Similarity 38.6%; Pred. No. 2.9e+02;
Matches 17; Conservative 9; Mismatches 13; Indels 5; Gaps 2;

QY 27 GKISKE---KSFLLVVELE-KLNIVAPDQLLEKLNHRIIDIK 65
DB 10 GKSKKPNGLKEFLSLEALKADLTLSKEELLELEKLNVAR 53

RESULT 9
T12832
hypothetical protein yonU - Bacillus subtilis phage SPBC2
C:Species: Bacillus subtilis phage SPBC2
C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C:Accession: T12832; D69915
R:Lazarevic, V.; Duesterhoef, A.; Soldo, B.; Hilbert, H.; Mauer, C.; Karamata, D.
submitted to the EMBL Data Library, August 1997
A:Description: The complete nucleotide sequence of the Bacillus subtilis SPbetac2 prophage
A:Reference number: Z17583
A:Accession: T12832
A:Status: preliminary; translated from GB/EMBL/DBSJ
A:Molecule type: DNA
A:Residues: 1-62 <LAZ>
A:Cross-references: UNIPROT:O64081; EMBL:AF020713; NID:g3025478; PID:g3025546; PIDN:AA011
C:Kunz, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertero
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chou
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritze, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallen
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Hleapfel, S.; Hosono, S.; Hulio, M.F.;
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidos, A.; Lardinois,
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel,
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle,
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Seror,
akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: D69915
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-62 <KUN>
A:Cross-references: GB:Z99115; GB:AL009126; NID:g2634478; PIDN:CAB14017.1; PID:e1183546;
A:Experimental source: strain 168
C:Genetics:
A:Gene: yonU

Query Match 12.7%; Score 47.5; DB 2; Length 62;
Best Local Similarity 35.0%; Pred. No. 3.4e+02;
Matches 14; Conservative 8; Mismatches 7; Indels 11; Gaps 2;

QY 32 EKSFLLVVELEKLNIVAPDQLLEKLNHRIIDIK 67
DB 2 EKFLDAIQQLTK-----ELEMKKLIDISKEATVRID 34

RESULT 10
S45688

glutathione transferase (EC 2.5.1.18), cardiac - human (fragments)
N/Alternate names: glutathione S-transferase
C:Species: Homo sapiens (man)
C>Date: 10-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C:Accession: S45688
R:Singhal, S.S.; Zimniak, P.; Awasthi, S.; Piper, J.T.; He, N.; Teng, J.I.; Petersen, D.
Arch. Biochem. Biophys. 311, 242-250, 1994
A>Title: Several closely related glutathione S-transferase isozymes catalyzing conjugati
A:Reference number: S45687; MUID:94263197; PMID:8203886
A:Accession: S45688
A:Molecule type: protein
A:Residues: 1-20;21-40 <SIN>
A:Cross-references: UNIPROT:Q9UDH3
C:Superfamily: glutathione transferase
C:Keywords: cardiac muscle; heart; transferase

Query Match 12.6%; Score 47; DB 2; Length 40;
Best Local Similarity 38.7%; Pred. No. 2.4e+02;
Matches 12; Conservative 11; Mismatches 6; Indels 2; Gaps 2;

QY 31 KEKSFDLVVELEKLNLVAPDQDLLEKCLK 61
DB 12 KEESY-DL-IKVEELSLYVNERPLLOAFIK 40

RESULT 11
C81372
very hypothetical protein Cj0974 [imported] - Campylobacter jejuni (strain NCTC 11168)
C:Species: Campylobacter jejuni
C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: C81372
R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel
Nature 403, 665-668, 2000
A>Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp
A:Reference number: A81250; MUID:20150912; PMID:10688204
A:Accession: C81372
A:Molecule type: DNA
A:Status: preliminary
A:Residues: 1-46 <PAR>
A:Cross-references: UNIPROT:Q9PNW4; GB:AL1139076; GB:AL111169; NID:g6968128; PIDN:CAB7323
A:Experimental source: serotype O2, strain NCTC 11168
C:Genetics:
A:Gene: Cj0974

Query Match 12.3%; Score 46; DB 2; Length 46;
Best Local Similarity 38.1%; Pred. No. 3.5e+02;
Matches 16; Conservative 7; Mismatches 17; Indels 2; Gaps 2;

QY 28 KISKESFDLVVELE-KLNLVAPDQDLLEKCLKNIHRIDL 68
DB 6 KIQVKSLDLVKKLNKQSLKIKNTNTKEN-LNKTHYLT 46

RESULT 12
F70225
hypothetical protein BBE11 - Lyme disease spirochete plasmid E/1p25
C:Species: Borrelia burgdorferi (Lyme disease spirochete)
C>Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C:Accession: F70225
R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A:Authors: Smith, H.O.; Venter, J.C.
A>Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A:Reference number: A70100; MUID:98065943; PMID:9403685
A:Accession: F70225
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-44 <KLE>
A:Cross-references: UNIPROT:O50707; GB:AE000785; NID:g2689951; PIDN:AAC66044.1; PID:g268
A:Experimental source: strain B31

C:Genetics:
A:Genome: plasmid

Query Match 12.2%; Score 45.5; DB 2; Length 44;
Best Local Similarity 27.5%; Pred. No. 3.7e+02;
Matches 11; Conservative 10; Mismatches 12; Indels 7; Gaps 1;

QY 31 KEKSFDLVVELEKLNLVAPDQDLLEKCLKNIHRIDLKT 70
DB 11 KEKDLIGIKIEKQK-----NLNVSRDNLKNMHLKLSKS 43

RESULT 13
D89871
conserved hypothetical protein SAS027 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: D89871
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, R.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A>Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: D89871
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-58 <KUR>
A:Cross-references: UNIPROT:Q99V64; GB:BA000018; PID:g13700831; PIDN:BAB42127.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: SAS027

Query Match 12.2%; Score 45.5; DB 2; Length 58;
Best Local Similarity 30.4%; Pred. No. 5e+02; 22; Indels 7; Gaps 3;

QY 11 SDVSLIFLMKDYMGR-GKISKESFDLVVELEKLNLVAPDQDLLEKCLKNIHR 65
DB 4 AEVGNIVEFMDGLGRVEKINDNSVIVDLTI-MENFN-----DLDPKPTVINHKR 53

RESULT 14
T12910
hypothetical protein vory - Bacillus subtilis phage SPBc2
C:Species: Bacillus subtilis phage SPBc2
C>Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C:Accession: T12910; A69925
R:Lazarevic, V.; Duesterhoeft, A.; Soldo, B.; Hilbert, H.; Maue, C.; Karamata, D.
submitted to the EMBL Data Library, August 1997
A>Description: The complete nucleotide sequence of the Bacillus subtilis SPbetac2 prophag
A:Reference number: Z17583
A:Accession: T12910
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-60 <LAZ>
A:Cross-references: UNIPROT:O64158; EMBL:AF020713; NID:g3025478; PID:g3025624; PIDN:AAAC1
R:Kunat, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi
A.; Enrich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall
iech, J.; Harwood, C.R.; Henaout, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.;
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parco, V.; Pohl, T.M.; Portetelle,
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, M.; Rose, M.; Sadate, Y.; Saco, T.; Scanlon,
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror,
keuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpsira, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A>Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377

A;Accession: A69925
A;Status: nucleic acid sequence not shown; translation not shown

Query Match 12.2%; Score 45.5; DB 2; Length 60;
Best Local Similarity 29.2%; Pred. No. 5.2e+02;

Qy 37 DLVVE-----LEKL-----NLVAPDQLDLEKCLNIHRIDLKTK 7

RESULT 15

ORF overlapping carboxyl terminus of IpaA - Shigella dysenteriae (fragment)

C:Species: Shigella dysenteriae
C:Date: 10-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 18-Nov-1994

CYACCESSION: B43859
R:Yao, R.; Palchaudhuri, S.
Infect. Immun. 60: 1163-1169. 1992

A,Accession: B43859
A>Status: preliminary

Query Match	Score 45;	DB 2;	Length 45;
Best 1000 simulations:	12.1%		
Best 1000 simulations:	25.1%	Best 1000 simulations:	25.1%

Query Match 12.1%; Score 45; DB 2; Length 45;

Best Local Similarity 35.1%; Pred. No. 4.3e+02;
Matches 13; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

Qy		29 ISKEKSFJDLVVELEKLNLVAPDQLDLEKCLKNIHR65 : : :
Dd		8 IOLKNNDITANNIYKAADVTTSLSKVLENINK44 :

db 8 ISDLKNNDDITAENNNIYKAADVTTLSKVLKNINK 44

Search completed: June 20, 2005, 13:22:38

Job time : 40 secs

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GenCore version 5.1.6
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QM protein - protein search, using sw model

Run on: June 20, 2005, 13:18:10 ; Search time 172 Seconds
(without alignments)
223.290 Million cell updates/sec

Title: US-10-713-208-6_COPY_1_75

Perfect score: 373

Sequence: 1 MAEIGEDLDKSDVSSLIPLM.....LEKCLKNHRLDKTKIQKY 75

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 résidues

Total number of hits satisfying chosen parameters: 148503

Minimum DB seq length: 0

Maximum DB seq length: 75

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	59	15.8	72	Q9AHY8	Q9ahy8 photorhabdu
2	56	15.0	60	1 DEGR_BACSU	P06563 bacillus su
3	54.5	14.6	73	2 Q6MSS7	Q6mss7 mycoplasma
4	53.5	14.3	59	1 MTPE SULAC	P62018 sulfolobus
5	53.5	14.3	59	1 MTPE SULTO	P62019 sulfolobus
6	53	14.2	59	2 Q9KEH2	Q9keh2 bacillus ha
7	53	14.2	64	2 Q8RI61	Q8ri61 fusbobacteri
8	53	14.2	66	2 Q8G3D6	Q8g3d6 brucella su
9	53	14.2	73	2 Q7RS48	Q7rs48 plasmodium
10	52	13.9	51	2 Q86256	Q86256 klebsiella
11	52	13.9	51	2 Q813F1	Q813f1 bacillus ce
12	51.5	13.8	45	2 Q9RSY9	Q9rsy9 thermotoga
13	51.5	13.8	67	2 Q63R79	Q63r79 bacillus ce
14	50.5	13.5	65	2 Q6XD88	Q6xd88 human rotav
15	50.5	13.5	66	2 Q8YEE6	Q8yee6 brucella me
16	50.5	13.5	68	2 Q31505	Q31505 bacillus su
17	50	13.4	75	2 Q7YW52	Q7yw52 echinococcu
18	49.5	13.3	70	1 YF79 METJA	Yf7952 methanococc
19	48.5	13.0	56	2 Q6L0E8	Q6ld88 homo sapien
20	48.5	13.0	66	1 RL29 HELPJ	Q9z191 helicobacte
21	48.5	13.0	66	2 Q22226	Q22226 arabidopsis
22	48.5	13.0	68	2 Q6F1D6	Q6f1d6 mesoplasma
23	48.5	13.0	75	2 Q8I4Q7	Q8i4q7 plasmodium
24	48	12.9	48	2 Q54872	Q54872 streptococc
25	48	12.9	52	1 YQAH_HAEIN	P56507 haemophilus
26	48	12.9	64	2 Q7P5D9	Q7p5d9 fusbobacteri
27	47.5	12.7	50	2 Q99PT2	Q99pt2 cavia porce
28	47.5	12.7	61	2 Q93AT0	Q93at0 pseudomonas
29	47.5	12.7	62	2 Q64081	Q64081 bacterioph
30	47.5	12.7	62	2 Q31940	Q31940 bacillus su
31	47.5	12.7	69	2 Q9TYA3	Q9tya3 caenorhabdi

32	47.5	12.7	71	2 Q6P456	Q6p456 homo sapien
33	47.5	12.7	74	2 Q6F0M2	Q6f0m2 mesoplasma
34	47	12.6	40	2 Q9UDH3	Q9udh3 homo sapien
35	47	12.6	40	2 Q9NBX3	Q9nbx3 acropora pa
36	47	12.6	74	2 Q65DR6	Q65dr6 bacillus li
37	46.5	12.5	56	2 Q8RG68	Q8rg68 fusbobacteri
38	46.5	12.5	62	2 Q6P965	Q6f965 acinetobact
39	46.5	12.5	62	2 Q7VGD6	Q7vgd6 helicobacte
40	46.5	12.5	71	2 Q89A09	Q89a09 clostridium
41	46.5	12.5	72	2 Q97T59	Q97t59 clostridium
42	46	12.3	46	2 Q9PNW4	Q9pnw4 campylobact
43	46	12.3	60	2 Q83291	Q83z91 enterococcu
44	46	12.3	63	2 Q7P9T7	Q7p9t7 rickettsia
45	46	12.3	69	2 Q7P2D8	Q7p2d8 fusbobacteri

ALIGNMENTS

RESULT 1
Q9AHY8 PRELIMINARY; PRT; 72 AA.
AC Q9AHY8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Lrp (fragment).
GN Name=lrp;
OS Photorhabdus luminescens (Xenorhabdus luminescens).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Photorhabdus.
OX NCBI_TaxID=29488;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NC19;
RX MEDLINE=21225535; PubMed=11325940;
RX DOI=10.1128/JB.183.10.3117-3126.2001;
RA Cliche T.A., Bintrim S.B., Horswill A.R., Ensign J.C.;
RT "A Phosphopantetheinyl transferase homolog is essential for
RT Photorhabdus luminescens to support growth and reproduction of the
RT entomopathogenic nematode Heterorhabditis bacteriophora.";
RL J. Bacteriol. 183:3117-3126(2001).
CC -|- SIMILARITY: Contains 1 HTH asnC-type DNA-binding domain.
DR EMBL; AF288086; AKL16099.1; -;
DR HSSP; P42180; I11G.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000485; HTH_AsnC_lrp.
DR InterPro; IPR009059; Wing_hlx_DNA_bnd.
DR Pfam; PF01037; AsnC_trans_reg; 1.
DR PRINTS; PR00033; HTHASNC.
DR SMART; SM00344; HTH_ASN_C.1.
DR PROSITE; PS00519; HTH_ASN_C_1; 1.
DR PROSITE; PS00956; HTH_ASN_C_2; 1.
KW DNA-binding; Transcription; Transcription regulation.
FT NON_TER 72 72
SQ SEQUENCE 72 AA; 8407 MW; 803932BD88EDB2DB CRC64;

Query Match 15.8%; Score 59; DB 2; Length 72;
Best Local Similarity 31.0%; Pred.No. 2.3e+02;
Matches 22; Conservative 11; Mismatches 20; Indels 18; Gaps 3;

QY	5	GEDLDKSDVSSLIPLMKYMGKSKSFLDVVLEKLNIVAPDQLDLLEKLNIIH 64							
Db	9	GKDLDRIDRNILNELQKD---GRISN-----VELSKRVGLSP-----FPCLERV 50							
QY	65	RIDLTKTIQKY 75							
Db	51	RLERQGFITGY 61							

RESULT 2

```
DEGR_BACSU STANDARD; PRT; 60 AA.
AC P06563;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Regulatory protein deGR.
GN Names=deGR; Synonyms=prTR; OrderedLocusNames=BSU21940;
OS Bacillus subtilis, and
OS Bacillus subtilis var. natto.
OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423, 86029;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=B.subtilis;
RX MEDLINE=87083406; PubMed=3098734;
RA Yang M., Shimotsu H., Ferrari E., Henner D.J.;
RT "Characterization and mapping of the Bacillus subtilis prTR gene.";
RL J. Bacteriol. 169:434-437(1987).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=B.subtilis; STRAIN=168 / Marburg;
RX MEDLINE=96349105; PubMed=8760912;
RA Sorokin A.V., Azevedo V., Zumstein E., Galleron N., Ehrlich S.D.,
RA Serror P.;
RT "Sequence analysis of the Bacillus subtilis chromosome region between
RT the serA and kdg loci cloned in a yeast artificial chromosome.";
RL Microbiology 142:2005-2016(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=B.subtilis; STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377; DOI=10.1038/36786;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borrisier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschini C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Entian K.-D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaeser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guiseppe G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M.,
RA Jones L.-M., Joris B., Karamata D., Kasahara Y., Klauer-Blanchard M.,
RA Klein C., Kobayashi Y., Koester P., Koningstein G., Krogh S.,
RA Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J.,
RA Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Mauel C.,
RA Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S.,
RA Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B.,
RA Park S.H., Parro V., Pohl T.M., Portetelle D., Porwollik S.,
RA Prescott A.M., Presecan E., Pujic P., Purnelle B., Rapoport G.,
RA Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B.,
RA Rose M., Sadale Y., Sato T., Scanlan E., Schleich S., Schroeter R.,
RA Scoffone F., Sekiguchi J., Sekowska A., Serror S.J., Serror P.,
RA Shin B.S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H.,
RA Takenaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P.,
RA Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F.,
RA Vassarotti A., Viari A., Wambutt R., Wedler E., Wedner H.,
RA Weitzenger T., Winters P., Wipat A., Yamamoto H., Yamane K.,
RA Yoshikawa H., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E.,
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis.";
RL Nature 390:249-256(1997).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=B.s.natto;
RX MEDLINE=86168015; PubMed=3082853;
RA Nagami Y., Tanaka T.;
RT "Molecular cloning and nucleotide sequence of a DNA fragment from
RT Bacillus natto that enhances production of extracellular proteases and
RT levanucrase in Bacillus subtilis.";
RL J. Bacteriol. 166:20-28(1986).
```

CC -!- FUNCTION: Leads, in B.subtilis, to enhanced production of
CC levanucrase, alkaline protease, and neutral protease. In B.natto
CC it is nonessential for growth or expression of proteases and
CC levanucrase.
CC
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CC
CC EMBL; M15318; AAA22672.1; -
CC EMBL; L77246; AAA96622.1; -
CC EMBL; Z99115; CAB14112.1; -
CC EMBL; M12917; AAA22671.1; -
CC PIR; I39957; I39957.
CC Subtilist; BG10699; deGR.
KW Complete proteome; Transcription regulation.
SQ SEQUENCE 60 AA; 7109 MW; C7B7F892FF0AB131 CRC64;

Query Match 15.0%; Score 56; DB 1; Length 60;
Best Local Similarity 27.8%; Pred. No. 3.8e+02;
Matches 15; Conservative 14; Mismatches 17; Indels 8; Gaps 1;

Qy 28 KISKSKSFLLDVVELEKLNVLAPDQLLEK-----CLKNIHRIIDLKTKIQ 73
Db 7 KULHKTFIEIYSDELEADIAKKGPKSMKYVEIEQRCKONILAIQMKIK 60

RESULT 3
Q6MSS7 PRELIMINARY; PRT; 73 AA.
AC Q6MSS7;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Hypothetical protein.
DE Hypothetical protein.
GN OrderedLocusNames=MSC_0692;
OS Mycoplasma mycoides (subsp. mycoides SC).
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=44101;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PG1;
RX PubMed=14762050; DOI=10.1101/gr.1673304;
RA Westberg J., Persson A., Holmberg A., Goessmann A., Lundeberg J.,
RA Johansson K.-E., Pettersson B., Uhlen M.;
RT "The genome sequence of Mycoplasma mycoides subsp. mycoides SC type
RT strain PG1T, the causative agent of contagious bovine pleuropneumonia
RT (CBPP)";
RL Genome Res. 14:221-227(2004).
DR EMBL; BX842644; CAE77311.1; -
DR GO; GO:0048037; F:cofactor binding; IEA.
DR InterPro; IPR009081; ACP like.
DR InterPro; IPR006163; Phosphatase_bind.
DR InterPro; IPR006162; Phosphatase_S.
DR Pfam; PF00550; PP-binding; 1.
DR PROSITE; PS00075; ACP DOMAIN; 1.
DR PROSITE; PS00012; PHOSPHOPANTHETINE; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 73 AA; 8309 MW; 1C923FBFC5633609 CRC64;

Query Match 14.6%; Score 54.5; DB 2; Length 73;
Best Local Similarity 33.3%; Pred. No. 6.5e+02;
Matches 19; Conservative 10; Mismatches 9; Indels 19; Gaps 4;

Qy 20 MKDYNGRGKISKEKSF-----LDLVVEL-EKLN-LVAPDQ-----DLLE 57
Db 11 LKSRGAKGNITKDSF-KSLGLDSLMDVMVTEKLNIRISDDQLSLRTDIDLK 67

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RESULT 4
ID MTPE SULAC STANDARD; PRT; 59 AA.
AC P62018; P23039;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Membrane-associated ATPase epsilon chain (EC 3.6.3.14) (Sul-ATPase
DE epsilon chain).
GN Name=atpE;
OS Sulfolobus acidocaldarius.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=2285;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=91072342; PubMed=2147683;
RA Denda K., Konishi J., Hajiro K., Oshima T., Date T., Yoshida M.;
RT "Structure of an ATPase operon of an acidothermophilic
RT archaeobacterium, Sulfolobus acidocaldarius.";
RL J. Biol. Chem. 265:21509-21513(1990).
CC -!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate +
CC H(+) (Out).
CC -!- SUBUNIT: Sul-ATPase is composed of six (or maybe five) subunits:
CC alpha, beta, delta, gamma, C (proteolipid), and possibly epsilon.
CC -!- SIMILARITY: Some, to E.hirae Ntph.
CC -----
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CC -----
DR EMBL; AP000986; BAB6506.1; -
KW Complete proteome; Hydrogen ion transport; Hydrolase.
SQ SEQUENCE 59 AA; 7038 MW; 4C07944C732225D4 CRC64;

Query Match 14.3%; Score 53.5; DB 1; Length 59;
Best Local Similarity 30.6%; Pred. No. 6.6e+02;
Matches 22; Conservative 14; Mismatches 17; Indels 19; Gaps 5;

QY 7 DLKSDVSLIFLMKDYMGKISKEKSFIDLVELEKLNL-----VAPQDLLEKLN 62
DB 3 EIDKSTIDKYINLK-----SKLDQKKNEL-----LSKINMEYEKTKQRLDELEKLN 52
QY 63 IHRIDLTKTIQK 74
DB 53 I-----LK-EVQK 59

RESULT 6
ID Q9KEH2 PRELIMINARY; PRT; 48 AA.
AC Q9KEH2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE BH0880 protein.
GN OrderedLocusNames=BH0880;
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=C-125;
RX MEDLINE=20512582; PubMed=11058132; DOI=10.1093/nar/28.21.4317;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331(2000).
DR EMBL; AF001510; BAB04599.1; -
DR FIR; H83759; H83759.
KW Complete proteome.
SQ SEQUENCE 48 AA; 5625 MW; CA22B6E9AD436AC0 CRC64;

Query Match 14.2%; Score 53; DB 2; Length 48;
Best Local Similarity 41.3%; Pred. No. 6e+02;
Matches 19; Conservative 6; Mismatches 11; Indels 10; Gaps 2;

QY 24 MGRGKISKEKSFIDLVELEKLNVLAPDQDLLEKLNHRIIDLK 69
DB 1 MGR-----KLLSFEELVLENKELNDPEQUSKIEK-----RUDEK 36

RESULT 5
ID MTPE SULTO STANDARD; PRT; 59 AA.
AC P62019; P23039;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Membrane-associated ATPase epsilon chain (EC 3.6.3.14) (Sul-ATPase
DE epsilon chain).
GN Name=atpE; OrderedLocusNames=STI1438.1; ORFNames=STSI172;
OS Sulfolobus tokodaii.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=111955;
RN [1]
SEQUENCE FROM N.A.
RX STRAIN=JCM 10545 / 7;
RX MEDLINE=21456156; PubMed=11572479;
RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
RA Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,
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RA Fraser C.M.;
RT "The Brucella suis genome reveals fundamental similarities between
RT animal and plant pathogens and symbionts.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
DR EMBL; AB014316; AAN28970.1; -.
DR TIGR; BR0012; -.
KW Complete proteome.
SQ SEQUENCE 66 AA; 7674 MW; FC12C02001F514AE CRC64;

Query Match 14.2%; Score 53; DB 2; Length 66;
Best Local Similarity 48.0%; Pred. No. 8.3e+02;
Matches 12; Conservative 5; Mismatches 4; Indels 4; Gaps 1;

QY 40 VELEKLNLV---APDQLDLEKLC 60
DB 24 IELEDLDVLRSIGPVDLDLMOECL 48

RESULT 9
Q7RS48 PRELIMINARY; PRT; 73 AA.
AC Q7RS48;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE Hypothetical protein.
GN Name=PY00517;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=17XNL;
RX PubMed=12368665; DOI=10.1038/nature01099;
RA Carlton J.M., Anguoli S.V., Suh B.B., Kooij T.W., Perteza M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,
RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RL parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -!- CAUTION: the sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABL01000144; EAA16610.1; -.
DR InterPro; IPR001388; Synaptobrevin.
DR PROSITE; PS50892; V SNARE; 1.
KW Hypothetical protein.
SQ SEQUENCE 73 AA; 8662 MW; BFE61FC8FB7D6527 CRC64;

Query Match 14.2%; Score 53; DB 2; Length 73;
Best Local Similarity 26.4%; Pred. No. 9.2e+02;
Matches 14; Conservative 11; Mismatches 28; Indels 0; Gaps 0;

QY 19 LMKDYNGRGKISKESFLDLVVELEKLNIVAPDQLDLEKLCNTHRIDLTKY 71
DB 1 MKRTLNLNKKCKDEKILAVKQKLNKINSVMNHNIDKLYESRGNIKALQYKTE 53

RESULT 10
O86256 PRELIMINARY; PRT; 51 AA.
ID O86256;
AC O86256;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Leucine responsive element (fragment).

Query Match 14.2%; Score 53; DB 2; Length 64;
Best Local Similarity 29.9%; Pred. No. 8.1e+02;
Matches 20; Conservative 14; Mismatches 13; Indels 20; Gaps 4;

QY 1 MARI-GEDLDKSVSLIFMK-----DYMGRGKISKESFLDLVVELEKLNIVA 49
DB 1 MABINGKYEINDVNLIDYLNKRYRVDRIWVDY--NGDIVKSDP-----EKINIKN 51

QY 50 PDQLDL 56
DB 52 TDKIEIV 58

RESULT 8
O8G3D6 PRELIMINARY; PRT; 66 AA.
ID O8G3D6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=BR0012;
OS Brucella suis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29461;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1330 / Biovar 1;
RX MEDLINE=22247741; PubMed=12271122; DOI=10.1073/pnas.192319099;
RA Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
RA Read T.D., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J.,
RA Daugherty S.C., DaBoy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
RA Nelson W.C., Ayodeji B., Kaul M., Shetty J., Malek J.A.,
RA Van Aken S.E., Riedmuller S., Tettelin H., Gill S.R., White O.,
RA Salzberg S.L., Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M.,
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GN Name=lrp;
OS Klebsiella oxytoca
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella
OX NCBI_TaxID=571;
RN [1]
RP SEQUENCE FROM N.A.
RA Albrecht C., Kleiner D.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y16963; CAAG565.1; -;
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000485; HTH_AsnC_lrp.
DR InterPro; IPR009058; wing_hix_DNA_bnd.
DR PRINTS; PRO0033; HTHASNC.
DR PROSITE; PS0956; HTH_ASN_C_2; 1.
FT NON_TER 51
SQ SEQUENCE 51 AA; 5857 MW; AE2B4C696F789F03 CRC64;

Query Match 13.9%; Score 52; DB 2; Length 51;
Best Local Similarity 32.8%; Pred. No. 8e+02;
Matches 20; Conservative 8; Mismatches 15; Indels 18; Gaps 3;

QY 5 GEDLDKSDVSSLIPLMKDYMGRGKISKESKSFLLDVVEKLNIVAPDQLDLLEKCLKNIH 64
DB 9 GKOLDRIDRILNLELQD-----GRISN-----VELSKRVGLSP-----TPCLERVX 50

QY 65 R 65
DB 51 R 51

RESULT 11
ID Q813F1 PRELIMINARY; PRT; 51 AA.
AC Q813F1;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical Cytoosolic Protein.
GN OrderedLocusNames=BC3144;
OS Bacillus cereus (strain ATCC 14579 / DSM 31).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=226900;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
RA Kapural V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,
RA Chu L., Mazur M., Goltzman E., Larsen N., D'Souza M., Walunas T.,
RA Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
RA Overbeek R., Kyrpides N.C.;
RT "Genome sequence of Bacillus cereus and comparative analysis with
RT Bacillus anthracis."
RL Nature 423:87-91(2003).
DR EMBL; AS017008; AAP10086.1; -;
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 51 AA; 5923 MW; C811DB6E5E6DA468 CRC64;

Query Match 13.9%; Score 52; DB 2; Length 51;
Best Local Similarity 39.4%; Pred. No. 8e+02;
Matches 13; Conservative 8; Mismatches 10; Indels 2; Gaps 2;

QY 10 KSDVSSLI-FLMKDYMGRGKISKESKFL-DLVV 40
DB 9 ESEISKATHWEKDYLGSGISVKTILRDML 41

RESULT 12
Q9RSY9
ID Q9RSY9 PRELIMINARY; PRT; 45 AA.
AC Q9RSY9;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE RNA polymerase sigma factor (Fragment).
OS Thermotoga maritima.
OC Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
OX NCBI_TaxID=2336;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93294870; PubMed=7685830;
RA Kim C.W., Markiewicz P., Lee J.J., Schierle C.F., Miller J.H.;
RT "Studies of the hyperthermophile Thermotoga maritima by random
RT sequencing of cDNA and genomic libraries. Identification and
RT sequencing of the trpEG (D) operon."
RL J. Mol. Biol. 231:960-981(1993).
DR HSSP; Q9EZJ8; 1KU2.
DR GO; GO:0016987; F:sigma factor activity; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0006352; P:transcription initiation; IEA.
DR InterPro; IPR007627; Sigma70_r2.
DR InterPro; IPR000943; Sigma70.
DR Pfam; PF04542; Sigma70_r2; 1.
DR PROSITE; PS00715; SIGMA70_1; 1.
FT NON_TER 1
FT NON_TER 45
SQ SEQUENCE 45 AA; 5049 MW; F8ED52EB456B12F5 CRC64;

Query Match 13.8%; Score 51.5; DB 2; Length 45;
Best Local Similarity 38.9%; Pred. No. 8e+02;
Matches 14; Conservative 6; Mismatches 11; Indels 5; Gaps 1;

QY 6 EDLDKSDVSSLIPLMKDYMGRGKISKESKSFLLDVE 41
DB 3 EKLITSNLRVLVSIKRYMGRG-----LSFQDLIQE 33

RESULT 13
Q63F79 PRELIMINARY; PRT; 67 AA.
ID Q63F79
AC Q63F79;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN ORFNames=B7ZK0829;
OS Bacillus cereus ZK.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=288681;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ZK;
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus cereus ZK."
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CP000001; AAU19413.1; -;
KW Hypothetical protein.
SQ SEQUENCE 67 AA; 7984 MW; AF1B680BF6DECA13 CRC64;

Query Match 13.8%; Score 51.5; DB 2; Length 67;
Best Local Similarity 36.1%; Pred. No. 1.2e+03;
Matches 13; Conservative 10; Mismatches 8; Indels 5; Gaps 2;

QY 38 LVVELEKLNIVAPDQLDLLEK-CLKNIHRIHLTKTI 72
DB 2 LILKVVVMKLEKELELELAKICKEN-----DLSTKL 33

RESULT 14
Q6XD88 PRELIMINARY; PRT; 65 AA.
ID Q6XD88


```
AC Q6XDB8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Nonstructural protein 1-3.
GN Names=NSP1-3;
OS Human rotavirus B.
OC Viruses; dsRNA viruses; Reoviridae; Rotavirus.
OX NCBI_TaxID=10942;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=Bang373;
RX MEDLINE=22996238; PubMed=14635024; DOI=10.1002/jmv.10546;
RA Ahmed M.U., Kobayashi N., Wakuda M., Sanekata T., Taniguchi K.,
RA Kader A., Naik T.N., Ishino M., Alam M.M., Kojima K., Mise K.,
RA Sumi A.;
RT "Genetic analysis of group B human rotaviruses detected in Bangladesh
RT in 2000 and 2001.";
RL J. Med. Virol. 72:149-155(2004).
DR EMBL; AY238391; AAQ18657.1; -.
DR GO; GO:0019012; C:virion; IEA.
KW Nonstructural protein.
SQ SEQUENCE 65 AA; 7400 MW; AB87B43E82262088 CRC64;

Query Match 13.5%; Score 50.5; DB 2; Length 65;
Best Local Similarity 27.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 14; Mismatches 27; Indels 5; Gaps 1;

QY 1 MABIGEDLDKSDVSSLIPLMKDYMGRGKISKESFLDLVVELEKLNLVAPDQDLLEKCL 60
Db | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
1 MTEKKAIIHSSNVAVIYIQGYLER-----ETSFSLSHVVPMTPLQLSWERLMTNVTY 55

QY 61 KNI 63
Db | :
56 QNL 58

RESULT 15
Q8YEE6 PRELIMINARY; PRT; 66 AA.
AC Q8YEE6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical Cytosolic Protein.
GN OrderedLocusNames=BMEI1932;
OS Brucella melitensis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29459;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=16M / ATCC 23456 / Biotype 1;
RX MEDLINE=20020109; PubMed=11756688; DOI=10.1073/pnas.221575398;
RA DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T.,
RA Ivanova N., Anderson I., Bhattacharya A., Lykidis A., Reznik G.,
RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltzman E.,
RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
RA Haselkorn R., Kyrpides N.C., Overbeek R.;
RT "The genome sequence of the facultative intracellular pathogen
RT Brucella melitensis.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
DR EMBL; AE009626; AAL51113.1; -.
DR PIR; AF3493; AF3493.
KW Complete proteome.
SQ SEQUENCE 66 AA; 7658 MW; E6C9AD8C01F514AE CRC64;

Query Match 13.5%; Score 50.5; DB 2; Length 66;
Best Local Similarity 31.2%; Pred. No. 1.5e+03;
Matches 15; Conservative 9; Mismatches 13; Indels 11; Gaps 2;

QY 24 MGRGKISKESFLDLVVEL-----EKNLV----APQDLLEKCL 60
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
```

Db 1 MORYRFDDKRILTEAIVELLNQIEPFDLDLVLSRIGPVDLDLMQECL 48

Search completed: June 20, 2005, 13:33:45

Job time : 175 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2005, 13:06:14 ; Search time 160 Seconds
(without alignments)
181.294 Million cell updates/sec

Title: US-10-713-208-6_COPY_1_75

Perfect score: 373

Sequence: 1 MAEIGEDLDKSDVSSLIPLM.....LSKCLKNHRIIDLKTKIQKY 75

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 1070894

Minimum DB seq length: 0

Maximum DB seq length: 75

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_16Dec04:.*
1: Geneseq1980s:.*
2: Geneseq1990s:.*
3: Geneseq2000s:.*
4: Geneseq2001s:.*
5: Geneseq2002s:.*
6: Geneseq2003as:.*
7: Geneseq2003bs:.*
8: Geneseq2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	75	20.1	55	2	AAY33287 Human FLI
2	63	16.9	27	2	Aay33286 Viral DED
3	63	16.9	27	2	Aay33289 Viral DED
4	61.5	16.5	64	6	AB99801 Amino aci
5	56	15.0	60	1	AAP71178 Bacillus
6	55	14.7	46	4	AAMI6687 Peptide #
7	55	14.7	46	4	ABB35670 Peptide #
8	55	14.7	46	4	AAM29171 Peptide #
9	55	14.7	46	4	ABB30505 Peptide #
10	55	14.7	46	4	ABB21099 Protein #
11	55	14.7	46	4	AAM68864 Human bon
12	55	14.7	46	4	AAM56485 Human bra
13	55	14.7	46	4	ABG50524 Human liv
14	55	14.7	46	4	AAM04403 Peptide #
15	55	14.7	46	5	ABG38444 Human pep
16	54	14.5	49	4	AAM20621 Peptide #
17	54	14.5	49	4	ABBA1825 Peptide #
18	54	14.5	49	4	AAM35621 Peptide #
19	54	14.5	49	4	ABB25545 Protein #
20	54	14.5	49	4	AAM75515 Human bon
21	54	14.5	49	4	AAM62697 Human bra
22	54	14.5	49	4	ABG57263 Human liv
23	54	14.5	49	5	ABG45071 Human pep
24	51.5	13.8	47	4	AAM09375 Thermotog
25	51	13.7	47	4	AAM09373 Staphyloc

26	49.5	13.3	62	5	ABP33224 Human ORF
27	49.5	13.3	71	4	AAM18411 Peptide #
28	49.5	13.3	71	4	ABB37453 Peptide #
29	49.5	13.3	71	4	AAM30888 Peptide #
30	49.5	13.3	71	4	ABB32201 Peptide #
31	49.5	13.3	71	4	ABB22746 Protein #
32	49.5	13.3	71	4	AAM70575 Human bon
33	49.5	13.3	71	4	AAM58128 Human bra
34	49.5	13.3	71	4	ABG52254 Human liv
35	49.5	13.3	71	4	AAM06010 Peptide #
36	49.5	13.3	71	5	ABG40238 Human pep
37	49	13.1	38	4	ABB37000 Peptide #
38	49	13.1	38	4	AAM70140 Human bon
39	49	13.1	38	4	ABG51850 Human liv
40	49	13.1	53	4	AAM17292 Peptide #
41	49	13.1	53	4	ABG51131 Human liv
42	49	13.1	53	4	AAM04977 Peptide #
43	49	13.1	68	2	AAM77599 Staphyloc
44	48.5	13.0	30	2	AAM45253 Peptide C
45	48.5	13.0	66	3	ABG60317 Arabidops

ALIGNMENTS

RESULT 1
AAY33287
ID AAY33287 standard; peptide; 55 AA;

XX AAY33287;

XX 23-NOV-1999 (first entry)

XX Human FLICE DED peptide fragment.

XX DED; death effector domain; FLICE protein; screening; anti-HHV-6;
KW viral envelope; apoptosis; multiple sclerosis; immunodeficient;
KW central nervous system; infection.

XX Homo sapiens.

OS DE19812182-A1.

XX 23-SEP-1999.

XX 19-MAR-1998; 98DE-01012182.

XX 19-MAR-1998; 98DE-01012182.

XX (FARB) BAYER AG.

XX Weber O, Hug H;

XX WPI; 1999-528902/45.

XX Identifying substances with anti-human herpes virus 6 activity useful for
XX treating multiple sclerosis and infections of the central nervous system.
XX Disclosure; Page 3; 4pp; German.

XX This invention describes a novel method to screen for effective anti-HHV-
XX 6 compounds which comprises incubating Fas-primed cells transfected with.
XX human herpes virus 6 (HHV-6) viral envelope or fragments of the viral
XX envelope with putative anti-HHV-6 compounds and examining the apoptotic
XX behaviour of the cells. The method is used to identify new anti-human
XX herpes virus 6 compounds, targeted to a death effector domain (DED)-
XX homologous region in HHV. These are effective for treating multiple
XX sclerosis and infections of the central nervous system, especially in
XX immunodeficient patients. This sequence represents a human FLICE protein
XX DED region which is used to describe the method of the invention
XX Sequence 55 AA;

```
Query Match      20.1%; Score 75; DB 2; Length 55;
Best Local Similarity 35.2%; Pred. No. 0.39;
Matches 19; Conservative 9; Mismatches 26; Indels 0; Gaps 0;

QY 3 EIGEDLDKSDVSSLIPLMKDYMGKISKEKSFSLDLIVLEKLNLVAPQDL 56
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB 2 DIGEQDSEDLASLKFLSLDYIPQRKEPTKDALMLFORLOEKRMLEESNLSFL 55

RESULT 2
AAY33286
ID AAY33286 standard; peptide; 27 AA.
XX AC AAY33286;
XX DT 23-NOV-1999 (first entry)
XX DE Viral DED domain competitive peptide.
XX KW DED domain; screening; anti-HIV; Fas-primed cell; viral envelope;
XX KW apoptosis; death effector domain; treatment; competitor; AIDS;
XX KW acquired immunodeficiency syndrome.
XX OS Synthetic.
XX DE19812181-A1.
XX PN 23-SEP-1999.
XX PF 19-MAR-1998; 98DE-01012181.
XX PR 19-MAR-1998; 98DE-01012181.
XX PA (FARB ) BAYER AG.
XX PI Weber O, Hug H;
XX WPI; 1999-528901/45.
XX PT Identifying substances with anti-HIV activity for treating acquired
XX PS immunodeficiency syndrome.
XX PS Disclosure; Col 3; 3pp; German.
XX CC This invention describes a novel method to screen for effective anti-HIV
XX CC compounds comprising Fas-primed cells transfected with human
XX CC immunodeficiency virus (HIV) viral envelope or fragments of the viral
XX CC envelope which are incubated with putative anti-HIV compounds and the
XX CC apoptotic behaviour of the cells is examined. The method is used to
XX CC identify new anti-HIV compounds, targeted to a death effector domain
XX CC (DED)-homologous region in HIV, that are effective for treating acquired
XX CC immunodeficiency syndrome. This sequence represents a peptide capable of
XX CC competitively binding to a viral DED domain
XX SQ Sequence 27 AA;

Query Match      16.9%; Score 63; DB 2; Length 27;
Best Local Similarity 50.0%; Pred. No. 4.3;
Matches 13; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 3 EIGEDLDKSDVSSLIPLMKDYMGK 28
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB 1 DIGEQDSEDLASLKFLSLDYIPQRK 26

RESULT 4
ABB99801
ID ABB99801 standard; protein; 64 AA.
XX AC ABB99801;
XX DT 07-APR-2003 (first entry)
XX DE Amino acid sequence of Plasmodium falciparum antigen DG747.
XX KW Antigen; DG747; interferon-gamma; sporozoite; immunogen; vaccine;
XX KW infection; malaria.
XX OS Plasmodium falciparum.
XX PN WO200292628-A2.
XX DT 21-NOV-2002.
XX PF 15-MAY-2002; 2002WO-FR001637.
XX PR 16-MAY-2001; 2001CA-02345206.
XX PR 23-MAY-2001; 2001CA-02346966.
XX
```

```
DE Viral DED domain competitive peptide.
XX DED; death effector domain; FLICE protein; screening; anti-HHV-6;
KW viral envelope; apoptosis; multiple sclerosis; immunodeficient;
KW central nervous system; infection.
XX OS Homo sapiens.
XX PN DE19812182-A1.
XX DT 23-SEP-1999.
XX PF 19-MAR-1998; 98DE-01012182.
XX PR 19-MAR-1998; 98DE-01012182.
XX PA (FARB ) BAYER AG.
XX PI Weber O, Hug H;
XX WPI; 1999-528902/45.
XX PT Identifying substances with anti-human herpes virus 6 activity useful for
XX PT treating multiple sclerosis and infections of the central nervous system.
XX PS Disclosure; Page 4; 4pp; German.
XX CC This invention describes a novel method to screen for effective anti-HHV-
XX CC 6 compounds which comprises incubating Fas-primed cells transfected with
XX CC human herpes virus 6 (HHV-6) viral envelope or fragments of the viral
XX CC envelope with putative anti-HHV-6 compounds and examining the apoptotic
XX CC behaviour of the cells. The method is used to identify new anti-human
XX CC herpes virus 6 compounds, targeted to a death effector domain (DED) -
XX CC homologous region in HHV. These are effective for treating multiple
XX CC sclerosis and infections of the central nervous system, especially in
XX CC immunodeficient patients. This sequence represents a peptide capable of
XX CC competitively binding to a viral DED domain
XX SQ Sequence 27 AA;

Query Match      16.9%; Score 63; DB 2; Length 27;
Best Local Similarity 50.0%; Pred. No. 4.3;
Matches 13; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 3 EIGEDLDKSDVSSLIPLMKDYMGK 28
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB 1 DIGEQDSEDLASLKFLSLDYIPQRK 26

RESULT 4
ABB99801
ID ABB99801 standard; protein; 64 AA.
XX AC ABB99801;
XX DT 07-APR-2003 (first entry)
XX DE Amino acid sequence of Plasmodium falciparum antigen DG747.
XX KW Antigen; DG747; interferon-gamma; sporozoite; immunogen; vaccine;
XX KW infection; malaria.
XX OS Plasmodium falciparum.
XX PN WO200292628-A2.
XX DT 21-NOV-2002.
XX PF 15-MAY-2002; 2002WO-FR001637.
XX PR 16-MAY-2001; 2001CA-02345206.
XX PR 23-MAY-2001; 2001CA-02346966.
XX
```

```
PA (INSP ) INST PASTEUR.
PI Drulhe P, Gruener A;
XX
XX WPI; 2003-129263/12.
XX N-PSDB; AB223335.
XX
XX New polynucleotide from Plasmodium falciparum and derived protein, useful
XX as immunogen for antimalarial vaccines and for preparing diagnostic or
XX therapeutic antibodies.
XX
XX Claim 5; Fig 1C; 115pp; French.
XX
XX The present sequence is a Plasmodium falciparum antigen, designated
XX DC747. This antigen generates an interferon-gamma response. The protein
XX is localised on the surface of sporozoites and on the intra-hepatic stage
XX of parasites. The antigen, as well as nucleic acids encoding it, is
XX useful as immunogens/vaccines for protection against infection by
XX Plasmodium falciparum. They are useful in treating P. falciparum malaria
XX and for in vitro diagnosis of infection
XX
XX Sequence 64 AA;
XX
Query Match 16.5%; Score 61.5; DB 6; Length 64;
Best Local Similarity 30.5%; Pred. No. 18;
Matches 18; Conservative 13; Mismatches 21; Indels 7; Gaps 2;
QY 18 FLMKDYMGKGI---SKEKSFLDLVVELEKLNVLVAPDQDLLEKCLKNHRIIDLKTKIQ 73
Db 2 FHMHDYIYDRIYNDKKN---VIKSDKNVKSNDKNKYCKNKNVKSNDKNVNIK 56
RESULT 5
AAP711178
ID AAP711178 standard; protein; 60 AA.
AC AAP711178;
XX
XX 25-MAR-2003 (revised)
XX 10-MAR-2003 (revised)
XX 15-APR-1991 (first entry)
XX
XX Bacillus exoprotease secretion promoting protein.
XX
XX Exoprotease.
XX
XX Bacillus sp.
XX
XX JP61282400-A.
XX
XX 12-DEC-1986.
XX
XX 07-JUN-1985; 85JP-00123736.
XX
XX 07-JUN-1985; 85JP-00123736.
XX
XX (MITU ) MITSUBISHI CHEM IND LTD.
XX
XX WPI; 1987-025820/04.
XX N-PSDB; AAN71310.
XX
XX Protein promoting extra:cellular prodn. of exo:protease - by use of
XX recombinant DNA technique.
XX
XX Claim 3; Page 1060; 8pp; Japanese.
XX
XX Protein may be produced from a bacterial expression vector, and has
XX extracellular exoprotease production promoting activity. (Updated on 10-
XX MAR-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct PA
XX field.)
XX
XX Sequence 60 AA;
XX
Query Match 15.0%; Score 56; DB 1; Length 60;
Best Local Similarity 27.8%; Pred. No. 72;
Matches 15; Conservative 14; Mismatches 17; Indels 8; Gaps 1;
QY 28 KISKEKSFLDLVVELEKLNVLVAPDQDLLEK-----CLKNHRIIDLKTKIQ 73
Db 7 KLJLHKTFFIYSDLEELADIAGKKGKPSMEKYVEEIQRCQKNILAIEIQMKIK 60
RESULT 6
AAM16687
ID AAM16687 standard; protein; 46 AA.
XX
XX AAM16687;
AC
XX 12-OCT-2001 (first entry)
XX
XX Peptide #3121 encoded by probe for measuring cervical gene expression.
XX
XX Probe; human; microarray; gene expression; cervical epithelial cell;
XX cervical cancer.
XX
XX Homo sapiens.
XX
XX WO200157278-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000670.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 03-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488901/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human cervical epithelial cells.
XX
XX Claim 27; SEQ ID NO 21513; 487pp; English.
XX
XX The present invention relates to human single exon nucleic acid probes
XX (SENP: see AAI10068-AA128459). The present sequence is a peptide encoded
XX by one such probe. The SENPs are derived from human Hela cells. The SENPs
XX can be used to produce a single exon microarray, which can be used for
XX measuring human gene expression in a sample derived from human cervical
XX epithelial cells. By measuring gene expression, the probes are therefore
XX useful in grading and/or staging of diseases of the cervix, notably
XX cervical cancer. Note: The sequence data for this patent did not form
XX part of the printed specification, but was obtained in electronic format
XX directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 46 AA;
XX
Query Match 14.7%; Score 55; DB 4; Length 46;
Best Local Similarity 30.6%; Pred. No. 69;
Matches 11; Conservative 12; Mismatches 13; Indels 0; Gaps 0;
QY 34 SFIDLVELEKLNVLVAPDQDLLEKCLKNHRIIDLK 69
Db 1 NLLDPIEMERKVRILGEGKLDILKRVCAQINKSLK 36
RESULT 7
ABB35670
```


Penn SG, Hanzel DK, Chen W, Rank DR;
WPI; 2001-496933/54.
New spatially-addressable set of single exon nucleic acid probes, useful
for measuring gene expression in sample derived from human breast,
comprises number of single exon nucleic acid probes.

Claim 27; SEQ ID NO 13473; 327pp + Sequence Listing; English.

The invention relates to a spatially-addressable set of single exon
nucleic acid probes for measuring gene expression in a sample derived
from human breast and Bt 474 cells. The method involves contacting the
probes with a collection of detectably labelled nucleic acids derived
from mRNA of human breast, and then measuring the label bound to each
probe of the microarray. The probes are useful for verifying the
expression of regions of genomic DNA predicted to encode proteins. They
are useful for gene discovery, and for determining predisposition and/or
prognosing breast disease. Gene expression analysis is useful for
assessing the toxicity of chemical agents on cells. The microarray of
this invention presents a far greater diversity of probes for measuring
gene expression, with far less bias than expressed sequence tag
microarrays. The method is suitable for rapid production of functional
information from genomic sequence. The present sequence is a peptide
encoded by a single exon nucleic acid probe of the invention. Note: The
sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format directly from WIPO
at ftp.wipo.int/pub/published_pct_sequences

Sequence 46 AA;

Query Match 14.7%; Score 55; DB 4; Length 46;
Best Local Similarity 30.6%; Pred. No. 69;
Matches 11; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

34 SFLLDVLVELEKLNVPQDLLEKLCNKNIHRIDLK 69
1 NLLDFIEMERKVILGEGKLILKRVCQAQINKSLK 36

RESULT 10
ABB21099
ID ABB21099 standard; protein; 46 AA.
XX
AC ABB21099;
XX
DT 23-JAN-2002 (first entry)
XX
DE Protein #3098 encoded by probe for measuring heart cell gene expression.
XX
KW Human; gene expression; heart; microarray; vascular system;
KW cardiovascular disease; hypertension; cardiac arrhythmia;
KW congenital heart disease.
XX
OS Homo sapiens.
XX
PN WO200157274-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000666.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
PT WPI; 2001-496933/54.
XX
PT New spatially-addressable set of single exon nucleic acid probes, useful
for measuring gene expression in sample derived from human breast,
comprises number of single exon nucleic acid probes.

Claim 27; SEQ ID NO 13473; 327pp + Sequence Listing; English.

The invention relates to a spatially-addressable set of single exon
nucleic acid probes for measuring gene expression in a sample derived
from human breast and Bt 474 cells. The method involves contacting the
probes with a collection of detectably labelled nucleic acids derived
from mRNA of human breast, and then measuring the label bound to each
probe of the microarray. The probes are useful for verifying the
expression of regions of genomic DNA predicted to encode proteins. They
are useful for gene discovery, and for determining predisposition and/or
prognosing breast disease. Gene expression analysis is useful for
assessing the toxicity of chemical agents on cells. The microarray of
this invention presents a far greater diversity of probes for measuring
gene expression, with far less bias than expressed sequence tag
microarrays. The method is suitable for rapid production of functional
information from genomic sequence. The present sequence is a peptide
encoded by a single exon nucleic acid probe of the invention. Note: The
sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format directly from WIPO
at ftp.wipo.int/pub/published_pct_sequences

Sequence 46 AA;

Query Match 14.7%; Score 55; DB 4; Length 46;
Best Local Similarity 30.6%; Pred. No. 69;
Matches 11; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

34 SFLLDVLVELEKLNVPQDLLEKLCNKNIHRIDLK 69
1 NLLDFIEMERKVILGEGKLILKRVCQAQINKSLK 36

RESULT 10
ABB21099
ID ABB21099 standard; protein; 46 AA.
XX
AC ABB21099;
XX
DT 23-JAN-2002 (first entry)
XX
DE Protein #3098 encoded by probe for measuring heart cell gene expression.
XX
KW Human; gene expression; heart; microarray; vascular system;
KW cardiovascular disease; hypertension; cardiac arrhythmia;
KW congenital heart disease.
XX
OS Homo sapiens.
XX
PN WO200157274-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000666.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
PT WPI; 2001-496933/54.
XX
PT New spatially-addressable set of single exon nucleic acid probes, useful
for measuring gene expression in sample derived from human breast,
comprises number of single exon nucleic acid probes.

Claim 27; SEQ ID NO 13473; 327pp + Sequence Listing; English.

The invention relates to a spatially-addressable set of single exon
nucleic acid probes for measuring gene expression in a sample derived
from human breast and Bt 474 cells. The method involves contacting the
probes with a collection of detectably labelled nucleic acids derived
from mRNA of human breast, and then measuring the label bound to each
probe of the microarray. The probes are useful for verifying the
expression of regions of genomic DNA predicted to encode proteins. They
are useful for gene discovery, and for determining predisposition and/or
prognosing breast disease. Gene expression analysis is useful for
assessing the toxicity of chemical agents on cells. The microarray of
this invention presents a far greater diversity of probes for measuring
gene expression, with far less bias than expressed sequence tag
microarrays. The method is suitable for rapid production of functional
information from genomic sequence. The present sequence is a peptide
encoded by a single exon nucleic acid probe of the invention. Note: The
sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format directly from WIPO
at ftp.wipo.int/pub/published_pct_sequences

Sequence 46 AA;

Query Match 14.7%; Score 55; DB 4; Length 46;
Best Local Similarity 30.6%; Pred. No. 69;
Matches 11; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

34 SFLLDVLVELEKLNVPQDLLEKLCNKNIHRIDLK 69
1 NLLDFIEMERKVILGEGKLILKRVCQAQINKSLK 36

RESULT 10
ABB21099
ID ABB21099 standard; protein; 46 AA.
XX
AC ABB21099;
XX
DT 23-JAN-2002 (first entry)
XX
DE Protein #3098 encoded by probe for measuring heart cell gene expression.
XX
KW Human; gene expression; heart; microarray; vascular system;
KW cardiovascular disease; hypertension; cardiac arrhythmia;
KW congenital heart disease.
XX
OS Homo sapiens.
XX
PN WO200157274-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000666.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
PT WPI; 2001-496933/54.
XX
PT New spatially-addressable set of single exon nucleic acid probes, useful
for measuring gene expression in sample derived from human breast,
comprises number of single exon nucleic acid probes.

Claim 27; SEQ ID NO 13473; 327pp + Sequence Listing; English.

The invention relates to a spatially-addressable set of single exon
nucleic acid probes for measuring gene expression in a sample derived
from human breast and Bt 474 cells. The method involves contacting the
probes with a collection of detectably labelled nucleic acids derived
from mRNA of human breast, and then measuring the label bound to each
probe of the microarray. The probes are useful for verifying the
expression of regions of genomic DNA predicted to encode proteins. They
are useful for gene discovery, and for determining predisposition and/or
prognosing breast disease. Gene expression analysis is useful for
assessing the toxicity of chemical agents on cells. The microarray of
this invention presents a far greater diversity of probes for measuring
gene expression, with far less bias than expressed sequence tag
microarrays. The method is suitable for rapid production of functional
information from genomic sequence. The present sequence is a peptide
encoded by a single exon nucleic acid probe of the invention. Note: The
sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format directly from WIPO
at ftp.wipo.int/pub/published_pct_sequences

Sequence 46 AA;

Query Match 14.7%; Score 55; DB 4; Length 46;
Best Local Similarity 30.6%; Pred. No. 69;
Matches 11; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

34 SFLLDVLVELEKLNVPQDLLEKLCNKNIHRIDLK 69
1 NLLDFIEMERKVILGEGKLILKRVCQAQINKSLK 36

RESULT 10
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ID ABB21099 standard; protein; 46 AA.
XX
AC ABB21099;
XX
DT 23-JAN-2002 (first entry)
XX
DE Protein #3098 encoded by probe for measuring heart cell gene expression.
XX
KW Human; gene expression; heart; microarray; vascular system;
KW cardiovascular disease; hypertension; cardiac arrhythmia;
KW congenital heart disease.
XX
OS Homo sapiens.
XX
PN WO200157274-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000666.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
PT WPI; 2001-496933/54.
XX
PT New spatially-addressable set of single exon nucleic acid probes, useful
for measuring gene expression in sample derived from human breast,
comprises number of single exon nucleic acid probes.

Claim 27; SEQ ID NO 13473; 327pp + Sequence Listing; English.

The invention relates to a spatially-addressable set of single exon
nucleic acid probes for measuring gene expression in a sample derived
from human breast and Bt 474 cells. The method involves contacting the
probes with a collection of detectably labelled nucleic acids derived
from mRNA of human breast, and then measuring the label bound to each
probe of the microarray. The probes are useful for verifying the
expression of regions of genomic DNA predicted to

GenCore version 5.1.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 20, 2005, 13:22:45 ; Search time 155 Seconds
(without alignments)
185.797 Million cell updates/sec

Title: US-10-713-208-6_COPY_1_75

Perfect score: 373

Sequence: 1 MAEIGEDLDKSDVSSLIFLM.....LSKCLKNIHRIDLTQYKIQY 75

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1714042 seqs, 383979560 residues

Total number of hits satisfying chosen parameters: 635259

Minimum DB seq length: 0

Maximum DB seq length: 75

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*
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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
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15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
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21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	277	74.3	56	15	US-10-627-571-7
3	237	63.5	56	15	US-10-627-571-6
4	225.5	60.5	59	15	US-10-627-571-4
5	99	26.5	75	14	US-10-001-254-31
6	90	24.1	75	9	US-09-952-768-66
7	90	24.1	75	15	US-10-668-955-66
8	79	21.2	56	15	US-10-627-571-9
9	74	19.8	72	14	US-10-001-254-34
10	68	18.2	56	15	US-10-627-571-8
11	61.5	16.5	64	17	US-10-712-533A-3

12	60	16.1	50	16	US-10-776-013-436	Sequence 436, App
13	56	15.0	57	17	US-10-489-123-13	Sequence 13, Appl
14	55	14.7	40	17	US-10-489-123-14	Sequence 14, Appl
15	55	14.7	46	9	US-09-864-761-36397	Sequence 36397, A
16	54	14.5	49	9	US-09-864-761-40843	Sequence 40843, A
17	53.5	14.3	72	17	US-10-489-123-12	Sequence 12, Appl
18	53	14.2	73	16	US-10-437-963-169508	Sequence 169508,
19	52.5	14.1	66	15	US-10-627-571-3	Sequence 3, Appli
20	52	13.9	65	15	US-10-424-599-164893	Sequence 164893,
21	52	13.9	68	16	US-10-425-115-185640	Sequence 185640,
22	52	13.9	70	15	US-10-424-599-244882	Sequence 244882,
23	51.5	13.8	47	9	US-09-823-266-15	Sequence 15, Appl
24	51.5	13.8	47	14	US-10-155-419-15	Sequence 15, Appl
25	51	13.7	47	9	US-09-823-266-13	Sequence 13, Appl
26	51	13.7	47	14	US-10-155-419-13	Sequence 13, Appl
27	50	13.4	53	15	US-10-424-599-181787	Sequence 181787,
28	50	13.4	59	15	US-10-335-977-8130	Sequence 8130, Ap
29	49.5	13.3	62	11	US-09-864-408A-4394	Sequence 4394, Ap
30	49.5	13.3	71	9	US-09-864-761-38044	Sequence 38044, A
31	49.5	13.3	75	16	US-10-767-701-50523	Sequence 50523, A
32	49	13.1	38	9	US-09-864-761-46700	Sequence 46700, A
33	49	13.1	53	9	US-09-864-761-46621	Sequence 46621, A
34	49	13.1	68	9	US-09-939-980-359	Sequence 359, App
35	49	13.1	71	16	US-10-437-963-183337	Sequence 183337,
36	49	13.1	72	16	US-10-425-115-241056	Sequence 241056,
37	48.5	13.0	66	9	US-09-815-242-11591	Sequence 11591, A
38	48.5	13.0	68	16	US-10-767-701-55846	Sequence 55846, A
39	48	12.9	50	17	US-10-690-276-570	Sequence 570, App
40	48	12.9	54	15	US-10-627-571-19	Sequence 19, Appl
41	48	12.9	66	16	US-10-856-499-1915	Sequence 1915, Ap
42	48	12.9	72	16	US-10-437-963-168063	Sequence 168063
43	47.5	12.7	47	9	US-09-823-266-14	Sequence 14, Appl
44	47.5	12.7	47	14	US-10-155-419-14	Sequence 14, Appl
45	47.5	12.7	51	14	US-10-097-065-620	Sequence 620, App

ALIGNMENTS

RESULT 1

US-10-627-571-5
; Sequence 5, Application US/10627571
; Publication No. US20040082771A1
; GENERAL INFORMATION:
; APPLICANT: KASID, Usha N.
; APPLICANT: KUMAR, Deepak
; APPLICANT: GOKHALE, Prafulla
; APPLICANT: AHMAD, Imran
; TITLE OF INVENTION: ANTI-APOTOPIC GENE SCC-S2 AND DIAGNOSTIC AND THERAPEUTIC USES
; FILE REFERENCE: 223316
; CURRENT APPLICATION NUMBER: US/10/627,571
; PRIOR FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US 60/264,062
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: PCT/US02/02212
; PRIOR FILING DATE: 2002-01-28
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: CASH Alpha/Beta - fragment
US-10-627-571-5

Query Match 74.3%; Score 277; DB 15; Length 56;
Best Local Similarity 100.0%; Pred. No. 46-24;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 SDVSSLIFLMKDYNGRGKLSKESFLDLVVELEKLNIVAPDQDLLEKCLKNIHRI 66

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Db      1 SDVSSLIFLMKDYMGKSKSEKSFDDLVELEKLNLVAPDQDLLEKCLKNHRI 56
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RESULT 2
US-10-627-571-7
; Sequence 7, Application US/10627571
; Publication No. US20040082771A1
; GENERAL INFORMATION:
; APPLICANT: KASID, Usha N.
; APPLICANT: KUMAR, Deepak
; APPLICANT: GOKHALE, Prafulla
; APPLICANT: AHMAD, Imran
; TITLE OF INVENTION: ANTI-APOTOPIC GENE SCC-S2 AND DIAGNOSTIC AND THERAPEUTIC USES
; FILE REFERENCE: 223316
; CURRENT APPLICATION NUMBER: US/10/627,571
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US 60/264,062
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: PCT/US02/02212
; PRIOR FILING DATE: 2002-01-28
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 7
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: FLIP (L) - fragment
US-10-627-571-7

Query Match      74.3%; Score 277; DB 15; Length 56;
Best Local Similarity 100.0%; Pred. No. 4e-24; Indels 0; Gaps 0;
Matches 56; Conservative 0; Mismatches 0;

QY      11 SDVSSLIFLMKDYMGKSKSEKSFDDLVELEKLNLVAPDQDLLEKCLKNHRI 66
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Db      1 SDVSSLIFLMKDYMGKSKSEKSFDDLVELEKLNLVAPDQDLLEKCLKNHRI 56
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RESULT 3
US-10-627-571-6
; Sequence 6, Application US/10627571
; Publication No. US20040082771A1
; GENERAL INFORMATION:
; APPLICANT: KASID, Usha N.
; APPLICANT: KUMAR, Deepak
; APPLICANT: GOKHALE, Prafulla
; APPLICANT: AHMAD, Imran
; TITLE OF INVENTION: ANTI-APOTOPIC GENE SCC-S2 AND DIAGNOSTIC AND THERAPEUTIC USES
; FILE REFERENCE: 223316
; CURRENT APPLICATION NUMBER: US/10/627,571
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US 60/264,062
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: PCT/US02/02212
; PRIOR FILING DATE: 2002-01-28
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 6
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Mus musculus
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: FLIP (L) - fragment
US-10-627-571-6

Query Match      63.5%; Score 237; DB 15; Length 56;
Best Local Similarity 80.4%; Pred. No. 1.5e-19;
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Matches 45; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY      11 SDVSSLIFLMKDYMGKSKSEKSFDDLVELEKLNLVAPDQDLLEKCLKNHRI 66
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Db      1 NDVSSLVFLTRDYGKGIADKSFDDLVELEKLNLIASDQNLLEKCLKNHRI 56
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RESULT 4
US-10-627-571-4
; Sequence 4, Application US/10627571
; Publication No. US20040082771A1
; GENERAL INFORMATION:
; APPLICANT: KASID, Usha N.
; APPLICANT: KUMAR, Deepak
; APPLICANT: GOKHALE, Prafulla
; APPLICANT: AHMAD, Imran
; TITLE OF INVENTION: ANTI-APOTOPIC GENE SCC-S2 AND DIAGNOSTIC AND THERAPEUTIC USES
; FILE REFERENCE: 223316
; CURRENT APPLICATION NUMBER: US/10/627,571
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US 60/264,062
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: PCT/US02/02212
; PRIOR FILING DATE: 2002-01-28
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 4
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Mus musculus
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: CASH Alpha/Beta - fragment
US-10-627-571-4

Query Match      60.5%; Score 225.5; DB 15; Length 59;
Best Local Similarity 76.3%; Pred. No. 3.2e-18;
Matches 45; Conservative 8; Mismatches 3; Indels 3; Gaps 1;

QY      11 SDVSSLIFL---MKDYMGKSKSEKSFDDLVELEKLNLVAPDQDLLEKCLKNHRI 66
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Db      1 NDVSSLVFLTRDYGKGIADKSFDDLVELEKLNLIASDQNLLEKCLKNHRI 59
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RESULT 5
US-10-001-254-31
; Sequence 31, Application US/10001254
; Publication No. US20030049702A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Godzik, Adam
; APPLICANT: Pawlowski, Krzysztof
; APPLICANT: Fiorentino, Loredana
; APPLICANT: Lee, Sug Hyung
; APPLICANT: Roth, Wilfred
; APPLICANT: Stenner-Liewen, Frank
; TITLE OF INVENTION: No. US20030049702A1el Death Domain Proteins
; FILE REFERENCE: P-LJ 5037
; CURRENT APPLICATION NUMBER: US/10/001,254
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/301,889
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/715,893
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-001-254-31
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; APPLICANT: Bartel, Paul
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING NEUROLOGICAL DISORDERS AND
; TITLE OF INVENTION: DISEASES
; FILE REFERENCE: 1600.24
; CURRENT APPLICATION NUMBER: US/10/776,013
; CURRENT FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 09/948904
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 09/466139
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/113534
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/124120
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/141243
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: 09/975072
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240790
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 10/194967
; PRIOR FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 60/304775
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 695
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 436
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-776-013-436

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Query Match 16.1%; Score 60; DB 16; Length 50;
Best Local Similarity 31.8%; Pred. No. 20;
Matches 14; Conservative 12; Mismatches 14; Indels 4; Gaps 1;

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US-10-489-123-13
; Sequence 13, Application US/10489123
; Publication No. US20050074463A1

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; GENERAL INFORMATION:
; APPLICANT: AUTRAN, BRIGITTE
; APPLICANT: SAMRI, ASSIA
; APPLICANT: DEBRE, PATRICE
; APPLICANT: CALVEZ, VINCENT
; APPLICANT: KATLAMA, CHRISTINE
; APPLICANT: HAAS, GABY
; TITLE OF INVENTION: THERAPEUTIC VACCINATION METHOD, MUTATED PEPTIDES OF HIV
; TITLE OF INVENTION: REVERSE TRANSCRIPTASE AND THEIR USE FOR VACCINATION AND
; TITLE OF INVENTION: REVERSE TRANSCRIPTASE AND THEIR USE FOR VACCINATION AND
; FILE REFERENCE: BDAC:007US
; CURRENT APPLICATION NUMBER: US/10/489,123
; CURRENT FILING DATE: 2004-03-12
; PRIOR APPLICATION NUMBER: PCT/FR01/02872
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-489-123-13

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Query Match 15.0%; Score 56; DB 17; Length 57;

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Best Local Similarity   31.9%; Pred. No. 68;
Matches 15; Conservative 12; Mismatches 16; Indels 4; Gaps 2;

QY      1  MABIGBDLKS---DYSSLIFLMKDYMGKGKISKSEKSFLDLVVELEK 44
       :|||::||::||::||::||::||::||::||::||::||::||
Db      5  LVEICAEEKEGKISALVVEICAELEKEGKISK-KALVEICAEEK 50

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US-10-489-123-14
; Sequence 14, Application US/10489123
; Publication No. US2005007463A1
; GENERAL INFORMATION:
; APPLICANT: AUTRAN, BRIGITTE
; APPLICANT: SAMRI, ASSIA
; APPLICANT: DEBRE, PATRICE
; APPLICANT: CALVEZ, VINCENT
; APPLICANT: KATLAWA, CHRISTINE
; APPLICANT: HAAS, GABY
; TITLE OF INVENTION: THERAPEUTIC VACCINATION METHOD, MUTATED PEPTIDES OF HIV
; TITLE OF INVENTION: REVERSE TRANSCRIPTASE AND THEIR USE FOR VACCINATION AND
; FILE REFERENCES: BDAC:007US
; CURRENT APPLICATION NUMBER: US/10/489,123
; CURRENT FILING DATE: 2004-03-12
; PRIOR APPLICATION NUMBER: PCT/FR01/02872
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 14
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-489-123-14
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Query Match 14.7%; Score 55; DB 17; Length 40;
Best Local Similarity 34.4%; Pred. No. 59;
Matches 11; Conservative 9; Mismatches 12; Indels

QY 13 VSSLIFLMDYMGKISKESFLDLVVELEK 44
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DB 2 IKALVEICAELEKEGKISKIKALVEICAELEK 33

RESULT 15
US-09-864-761-36397
; Sequence 36397, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aescmica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
; SEQ ID NO 36397
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC007256.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.6
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 4
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.9
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.5
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 4
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.5
; OTHER INFORMATION: EST HUMAN HIT: BF095670.1, EVALUE 9.00e-19
; OTHER INFORMATION: SWISSPROT HIT: Q14790, EVALUE 7.00e-20
US-09-864-761-36397

Query Match 14.7%; Score 55; DB 9; Length 46;
Best Local Similarity 30.6%; Pred. No. 69;
Matches 11; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

QY 34 SFLLDLVVELEKLNVLAPDOLDLEKCLKNIHRIDLK 69
Db 1 NLLDIFIEKRVILGEGKLDILKRVCAQINKSLK 36

Search completed: June 20, 2005, 13:38:15
Job time : 156 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2005, 13:19:14 ; Search time 42 Seconds
(without alignments)
133.302 Million cell updates/sec

Title: US-10-713-208-6_COPY_1_75
Perfect score: 373
Sequence: 1 MAEIGBDLKDVSLLFLM.....LEKLNHRIIDLTKIQKY 75

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 302356

Minimum DB seq length: 0
Maximum DB seq length: 75

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/ptodata/1/iaa/5A COMB pep.*
2: /cgn2_6/ptodata/1/iaa/5B COMB pep.*
3: /cgn2_6/ptodata/1/iaa/6A COMB pep.*
4: /cgn2_6/ptodata/1/iaa/6B COMB pep.*
5: /cgn2_6/ptodata/1/iaa/PTUS COMB pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	99	26.5	75	1 US-08-665-220-66	Sequence 66, Appl
2	91	24.4	68	4 US-09-180-167A-13	Sequence 13, Appl
3	91	24.4	68	4 US-09-033-524B-13	Sequence 13, Appl
4	90	24.1	75	3 US-09-291-692-66	Sequence 66, Appl
5	90	24.1	75	4 US-09-952-768-66	Sequence 66, Appl
6	80	21.4	66	4 US-09-180-167A-12	Sequence 12, Appl
7	80	21.4	66	4 US-09-033-524B-12	Sequence 12, Appl
8	69	18.5	64	4 US-09-180-167A-31	Sequence 31, Appl
9	69	18.5	64	4 US-09-033-524B-31	Sequence 31, Appl
10	66	17.7	67	4 US-09-180-167A-10	Sequence 10, Appl
11	66	17.7	67	4 US-09-033-524B-10	Sequence 10, Appl
12	51.5	13.8	47	4 US-09-823-266-15	Sequence 15, Appl
13	51	13.7	47	4 US-09-823-266-13	Sequence 13, Appl
14	51	13.7	47	4 US-09-180-167A-11	Sequence 11, Appl
15	51	13.7	47	4 US-09-033-524B-11	Sequence 11, Appl
16	50.5	13.5	69	4 US-09-621-976-7353	Sequence 7353, Ap
17	49	13.1	54	4 US-09-621-976-4976	Sequence 4976, Ap
18	49	13.1	68	3 US-08-936-165A-359	Sequence 359, App
19	49	13.1	72	4 US-09-621-976-7354	Sequence 7354, Ap
20	48.5	13.0	70	3 US-09-367-953B-107	Sequence 107, App
21	48.5	13.0	72	4 US-09-270-767-32287	Sequence 32287, A
22	48.5	13.0	72	4 US-09-270-767-47504	Sequence 47504, A
23	48	12.9	66	4 US-09-640-211A-1915	Sequence 1915, Ap
24	48	12.9	67	2 US-08-142-551B-9	Sequence 9, Appli
25	47.5	12.7	47	4 US-09-823-266-14	Sequence 14, Appl
26	47	12.6	66	2 US-08-867-087B-40	Sequence 40, Appl
27	46	12.3	41	3 US-08-974-549A-181	Sequence 181, App

Sequence 181, App
Sequence 181, App
Sequence 4, Appli
Sequence 4, Appli
Sequence 25750, A
Sequence 24519, A
Sequence 3, Appli
Sequence 40620, A
Sequence 55836, A
Sequence 89, Appl
Sequence 829, App
Sequence 7547, Ap
Sequence 460, App
Sequence 276, App
Sequence 277, App
Sequence 277, App
Sequence 276, App

41 4 US-09-402-181B-181
41 4 US-09-721-456-181
49 3 US-09-382-155-4
49 3 US-09-074-044A-4
61 4 US-09-248-796A-25750
71 4 US-09-248-796A-24519
73 4 US-09-125-635-3
68 4 US-09-270-767-40620
68 4 US-09-270-767-55836
34 4 US-09-843-221A-89
66 4 US-09-732-210-829
70 4 US-09-543-681A-7547
75 3 US-08-858-207A-460
35 3 US-09-082-279B-276
35 3 US-09-082-279B-277
35 3 US-09-315-304B-276
35 4 US-09-834-784-276

ALIGNMENTS

RESULT 1
US-08-665-220-66
; Sequence 66, Application US/08665220
; Patent No. 5786173
; GENERAL INFORMATION:
; APPLICANT: Alnemti, Emad S.
; APPLICANT: Fernandes-Alnemti, Teresa
; APPLICANT: Litwack, Gerald
; APPLICANT: Armstrong, Robert
; APPLICANT: Tomaselli, Kevin
; TITLE OF INVENTION: Mch4 and Mch5, Apoptotic Proteases,
; TITLE OF INVENTION: Nucleic Acids Encoding and Methods of Use
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,220
; FILING DATE: 14-JUN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/618,408
; FILING DATE: 19-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 75 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..75
; OTHER INFORMATION: /note="Mch5 A"
; US-08-665-220-66


```
RESULT 9
US-09-033-524B-31
; Sequence 31, Application US/09033524B
; Patent No. 6607880
; GENERAL INFORMATION:
; APPLICANT: Gordon C. Shore et al.
; TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING
; FILE REFERENCE: 50013/004002
; CURRENT APPLICATION NUMBER: US/09/033,524B
; CURRENT FILING DATE: 1998-03-02
; PRIOR APPLICATION NUMBER: CA 2,198,988
; PRIOR FILING DATE: 1997-03-03
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-033-524B-31

Query Match      18.5%; Score 69; DB 4; Length 64;
Best Local Similarity 30.9%; Pred. No. 0.26;
Matches 17; Conservative 11; Mismatches 23; Indels 4; Gaps 1;

QY      3  EIGEDLDKSDVSSLIFFLMKDYMGKISKEKSFGLDLVVELEKLNLVAPDQDLLE 57
         |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      11  ELSEGIDSENKDMIFLLKDSLPK-----TMTSLSLFLAEKQKIDEDNLTCL 61

RESULT 10
US-09-180-167A-10
; Sequence 10, Application US/09180167A
; Patent No. 6558950
; GENERAL INFORMATION:
; APPLICANT: Gordon C. Shore et al.
; TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING
; FILE REFERENCE: 50013/004003
; CURRENT APPLICATION NUMBER: US/09/180,167A
; CURRENT FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: CA 2,198,988
; PRIOR FILING DATE: 1997-03-03
; PRIOR APPLICATION NUMBER: PCT/IB98/00706
; PRIOR FILING DATE: 1998-03-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-180-167A-10

Query Match      17.7%; Score 66; DB 4; Length 67;
Best Local Similarity 29.8%; Pred. No. 0.65;
Matches 17; Conservative 13; Mismatches 27; Indels 0; Gaps 0;

QY      4  IGEDLDKSDVSSLIFFLMKDYMGKISKEKSFGLDLVVELEKLNLVAPDQDLLEKCL 60
         :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      11  VSSLSSELTELKFLCLGRVGRKRLERVQSGLDLFSMLLEQNDLEPGHTELLRELL 67

RESULT 11
US-09-033-524B-10
; Sequence 10, Application US/09033524B
; Patent No. 6607880
; GENERAL INFORMATION:
; APPLICANT: Gordon C. Shore et al.
; TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING
; FILE REFERENCE: 50013/004002
; CURRENT APPLICATION NUMBER: US/09/033,524B
; CURRENT FILING DATE: 1998-03-02
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; PRIOR APPLICATION NUMBER: CA 2,198,988
; PRIOR FILING DATE: 1997-03-03
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-033-524B-10

Query Match      17.7%; Score 66; DB 4; Length 67;
Best Local Similarity 29.8%; Pred. No. 0.65;
Matches 17; Conservative 13; Mismatches 27; Indels 0; Gaps 0;

QY      4  IGEDLDKSDVSSLIFFLMKDYMGKISKEKSFGLDLVVELEKLNLVAPDQDLLEKCL 60
         :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      11  VSSLSSELTELKFLCLGRVGRKRLERVQSGLDLFSMLLEQNDLEPGHTELLRELL 67

RESULT 12
US-09-823-266-15
; Sequence 15, Application US/09823266
; Patent No. 6613531
; GENERAL INFORMATION:
; APPLICANT: Burgess, Richard
; APPLICANT: Arthur, Terrance
; APPLICANT: Anthony, Larry
; APPLICANT: Bergendahl, Viet
; APPLICANT: Pietz, Bradley
; TITLE OF INVENTION: Sigma binding region of RNA polymerase and uses thereof
; FILE REFERENCE: 800.025US1
; CURRENT APPLICATION NUMBER: US/09/823,266
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 60/193,116
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 47
; TYPE: PRT
; ORGANISM: T. maritima
US-09-823-266-15

Query Match      13.8%; Score 51.5; DB 4; Length 47;
Best Local Similarity 38.9%; Pred. No. 26;
Matches 14; Conservative 6; Mismatches 11; Indels 5; Gaps 1;

QY      6  EDLDKSDVSSLIFFLMKDYMGKISKEKSFGLDLVVE 41
         ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      8  EKLITSNLRVSVIAKRYMGRG-----LSFQDLIOE 38

RESULT 13
US-09-823-266-13
; Sequence 13, Application US/09823266
; Patent No. 6613531
; GENERAL INFORMATION:
; APPLICANT: Burgess, Richard
; APPLICANT: Arthur, Terrance
; APPLICANT: Anthony, Larry
; APPLICANT: Bergendahl, Viet
; APPLICANT: Pietz, Bradley
; TITLE OF INVENTION: Sigma binding region of RNA polymerase and uses thereof
; FILE REFERENCE: 800.025US1
; CURRENT APPLICATION NUMBER: US/09/823,266
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 60/193,116
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 47
; TYPE: PRT
```

ORGANISM: S. aureus
US-09-823-266-13

Query Match 13.7%; Score 51; DB 4; Length 47;
Best Local Similarity 31.0%; Pred. No. 30;
Matches 13; Conservative 11; Mismatches 8; Indels 10; Gaps 2;

QY 5 GEDLDKSDVSS-----LIFLMKDYMGKISKESFLDLVVE 41
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 2 GDEVAKSRLAEANLRLVLSIAKRYVGRGML-----FLDLIQE 38

RESULT 14
US-09-180-167A-11
; Sequence 11, Application US/09180167A
; Patent No. 6558950
; GENERAL INFORMATION:
; APPLICANT: Gordon C. Shore et al.
; TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING
; TITLE OF INVENTION: APOPTOSIS
; FILE REFERENCE: 50013/004003
; CURRENT APPLICATION NUMBER: US/09/180,167A
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: CA 2,198,988
; PRIOR FILING DATE: 1997-03-03
; PRIOR APPLICATION NUMBER: PCT/IB98/00706
; PRIOR FILING DATE: 1998-03-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-180-167A-11

Query Match 13.7%; Score 51; DB 4; Length 67;
Best Local Similarity 28.3%; Pred. No. 46;
Matches 15; Conservative 12; Mismatches 26; Indels 0; Gaps 0;

QY 8 LDKSDVSSLIFLMKDYMGKISKESFLDLVVELEKLNLVAPDQDLLEKCL 60
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 15 LSGNDLMELKFLCRERVSKRLERVQSGLDLFTVLLQNDLGRHTGLLELL 67

RESULT 15
US-09-033-524B-11
; Sequence 11, Application US/09033524B
; Patent No. 6607880
; GENERAL INFORMATION:
; APPLICANT: Gordon C. Shore et al.
; TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING
; TITLE OF INVENTION: APOPTOSIS
; FILE REFERENCE: 50013/004002
; CURRENT APPLICATION NUMBER: US/09/033,524B
; CURRENT FILING DATE: 1998-03-02
; PRIOR APPLICATION NUMBER: CA 2,198,988
; PRIOR FILING DATE: 1997-03-03
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-033-524B-11

Query Match 13.7%; Score 51; DB 4; Length 67;
Best Local Similarity 28.3%; Pred. No. 46;
Matches 15; Conservative 12; Mismatches 26; Indels 0; Gaps 0;

QY 8 LDKSDVSSLIFLMKDYMGKISKESFLDLVVELEKLNLVAPDQDLLEKCL 60
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 15 LSGNDLMELKFLCRERVSKRLERVQSGLDLFTVLLQNDLGRHTGLLELL 67

Search completed: June 20, 2005, 13:34:31
Job time : 43 secs

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Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	73.5	7.9	149	2	T43637	casepase protein 1C
2	70.5	7.6	135	2	A93222	hypothetical prote
3	69	7.4	152	2	A93355	hypothetical prote
4	68.5	7.4	136	2	T08216	outer arm dynein 1
5	68	7.3	137	1	JC4233	lysozyme (EC 3.2.1
6	67	7.2	125	2	AD0297	probable membrane
7	65.5	7.0	164	2	T16321	hypothetical prote
8	64.5	6.9	89	2	E47758	retrovirus-related
9	64.5	6.9	114	2	T19229	hypothetical prote
10	64.5	6.9	174	2	H71267	conserved hypothet
11	63.5	6.8	167	2	S34363	hypothetical prote
12	63.5	6.8	171	2	A11060	probable acetyltra
13	63	6.8	172	2	E82053	probable fibribial
14	61.5	6.6	156	2	H86672	hypothetical prote
15	61.5	6.6	160	2	E82382	transcription regu
16	61	6.6	149	1	E69073	NADP-reducing hydr
17	61	6.6	160	2	H75062	flagella-related p
18	60.5	6.5	99	2	A70366	hypothetical prote
19	60	6.5	136	2	I51222	neurotrophin recept
20	60	6.5	137	2	S76052	hypothetical prote
21	59.5	6.4	154	2	F81917	hypothetical prote
22	59.5	6.4	156	2	T12893	hypothetical prote
23	58.5	6.3	120	2	E70479	dnak suppressor pr
24	58.5	6.3	146	2	AD2258	hypothetical prote
25	58.5	6.3	153	2	A87732	protein W10C8.4 [li
26	58.5	6.3	157	2	S35486	xylS protein - Fse
27	58.5	6.3	159	2	C97071	phosphoribosylcarb
28	58.5	6.3	165	2	AB2113	hypothetical prote
29	58	6.2	118	2	T14570	cvtochrome b559 co

C; Superf

Query Match 7.6%; Score 70.5; DB 2; Length 135; Best Local Similarity 33.8%; Pred. No. 17; Matches 25; Conservative 15; Mismatches 27; Indels 7; Gaps 4;

QY 4 VQAGTGYRNVLQAATQKSLKDPNS--NPREPVKKSIOESEA-FLPQSIPEERYKMK 59
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
DB 26 VQYKGS--RLLLSVVESSPDDESSADPMVSPAVAKLRDAQALFLOQGIPEIVEKQ 83
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
QY 60 KP-LGICLIIDCIG 72
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
DB 84 KPFTICDVADEIG 97
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :

RESULT 3
A97355
hypothetical protein CAC3708 [imported] - Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C:Accession: A97355
R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clostridium acetobutylicum
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: A97355
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-152 <KUR>
A:Cross-references: UNIPROT:Q97CV2; GB:AE001437; PIDN:AAK81628.1; PID:g15026813; GSPDB:G15026813
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC3708

Query Match 7.4%; Score 69; DB 2; Length 152; Best Local Similarity 28.3%; Pred. No. 28; Matches 22; Conservative 16; Mismatches 26; Indels 12; Gaps 2;

QY 19 IQKSLKDPNSNPREPVKKSIOESEAFLPQSIPEERYKMKSLGICLIIDCIGNTELL 78
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
DB 86 LKALDAPTAKKKEFPVKIVETAMPKAEAVKVPKSTP-----VKKEPENP 136
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
QY 79 RDTFTSL---GYEVQK 91
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
DB 137 YDPFYKLKHKKEVKK 152
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :

RESULT 4
T08216
outer arm dynein light chain, 19K - Chlamydomonas reinhardtii
C:Species: Chlamydomonas reinhardtii
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: T08216
R:Patel-King, R.S.; Benashski, S.E.; Harrison, A.; King, S.M.
J. Cell Biol. 137, 1081-1090, 1997
A:Title: A Chlamydomonas homolog of the putative murine t complex distorter Tctex-2 is a member of the dynein light chain family
A:Reference number: Z16406; MUID:97311077; PMID:9166408
A:Accession: T08216
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-136 <PAT>
A:Cross-references: UNIPROT:O04355; EMBL:U89649; NID:g2138333; PID:g2138334
A:Experimental source: strain 1132D

Query Match 7.4%; Score 68.5; DB 2; Length 136; Best Local Similarity 22.6%; Pred. No. 27; Matches 26; Conservative 28; Mismatches 40; Indels 21; Gaps 5;

QY 6 GAGTSY-RNVLQAATQKSLKDPNSNPREPVK-----KSIQSEAFLPQSIPEERYKM-- 57
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
DB 28 GPNTEERHKVQAVLQVKLERTEKQYDPVKGAQISKQLADDLREKVKALGYDRYKLV 87
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
QY 58 -----KSKPLGICLIIDCIGNTELLRDTFTSLGYEVQKFLHLSMHGISQILGQF 107
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :

DB 88 QVTGQKQGMRIIRCLWDQT---NDFASEYYENE-----SMYCVQCVYGLY 134
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
RESULT 5
JC4233
lysozyme (EC 3.2.1.17) precursor - silkworm
C:Species: Bombyx mori (silkworm)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: JC4233; PC4067
R:Lee, W.J.; Brey, P.T.
Gene 161, 199-203, 1995
A:Title: Isolation and characterization of the lysozyme-encoding gene from the silkworm Bombyx mori
A:Reference number: JC4233; MUID:95394356; PMID:7665079
A:Accession: JC4233
A:Molecule type: mRNA
A:Residues: 1-137 <LEE>
A:Cross-references: UNIPROT:P48816; GB:L37416; NID:9567098; PIDN:AAB40947.1; PID:g567099
A:Accession: PC4067
A:Molecule type: protein
A:Residues: 19-24; 40-45 <LE2>
C:Comment: This enzyme catalyzes the hydrolysis of the beta-1,4-glycosidic linkage between d cuticular epidermal tissue following the injection of Gram positive bacteria.
C:Comment: This protein has eight structural important cysteine residues.
C:Genetics:
A:Gene: lys
C:Superfamily: lysozyme c
C:Keywords: bacteriolytic enzyme; glycosidase; hydrolase; polysaccharide degradation
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-137/Product: lysozyme #status predicted <MAT>
F:50,67/Active site: Glu, Asp #status predicted

Query Match 7.3%; Score 68; DB 1; Length 137; Best Local Similarity 28.0%; Pred. No. 31; Matches 21; Conservative 16; Mismatches 24; Indels 14; Gaps 5;

QY 66 LIIDCIGNTELLRDTFTSLG--YEVQKFLHLSMHGISQ-ILGQFACMPPEHRDYSFVCV 122
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
DB 9 LVVLGVGSEAK---TFTRCGLVHLRK-----HGFEENLMRNWVCLVEHSSRDTSKT 58
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
QY 123 LVSRGGSQSVGVQDQ 137
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
DB 59 NTRNGSKD-YGLFQ 72
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :

RESULT 6
AD0297
probable membrane protein YPO2435 [imported] - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C:Accession: AD0297
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Gil, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall, I.; Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AD0297
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-125 <KUR>
A:Cross-references: UNIPROT:Q8ZDW3; GB:AL590842; PIDN:CAC91240.1; PID:g15980429; GSPDB:G15980429
C:Genetics:
A:Gene: YPO2435

Query Match 7.2%; Score 67; DB 2; Length 125; Best Local Similarity 25.0%; Pred. No. 34; Matches 17; Conservative 10; Mismatches 15; Indels 26; Gaps 2;

QY 86 GYEYQKFLHLSMHGISQILGQFACMP-----HRDYSFV----- 120
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
DB 26 GYQLAKFRVMSHSGQAIDKKSKCLPRTPDPAPHRVYISFVNVHNSAKNDLHYRLLLLSA 85
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :


```
QY 121 -CVLVRG 127
Db 86 GCIASTG 93

RESULT 7
T16321
hypothetical protein F41C6.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T16321
R:Geisel, C.
submitted to the EMBL Data Library, October 1995
A:Description: The sequence of C. elegans cosmid F41C6.
A:Reference number: Z18495
A:Accession: T16321
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-164 <CE1>
A:Cross-references: UNIPROT:Q20267; EMBL:U39745; NID:g1049470; PID:g1049471; PIDN:AAA804
C:Genetics:
A:Gene: CBSP:F41C6.2
A:Introns: 51/3; 67/1

Query Match 7.0%; Score 65.5; DB 2; Length 164;
Best Local Similarity 23.2%; Pred. No. 66;
Matches 32; Conservative 16; Mismatches 39; Indels 51; Gaps 6;

QY 61 PLGICLII-----DCIGN-----ETELLRTFTSLGVEVQKFLHLSM 97
Db 7 PLRSCLTIYVNCDCFNLRNSVVICVDVSRKKEVPDWMKEKAPAGLLISLMEHLSS 66

QY 98 HGISQILQGFACMPHEHRDVSFCVL-----VSRGGSQSYGVVDQT-----HSLGLPLH 145
Db 67 VGLAQVYGRV-----EQAYKEDQVLEGAQVYEGFTQYARVDQYVVRVALDHTGSPIS 121

QY 146 HIRRMFMGDCPVLACKP 163
Db 122 N-----WILGKP 128

RESULT 8
E47758
retrovirus-related reverse transcriptase homolog - Liriodendron chinense retrotransposon
C:Species: Liriodendron chinense
C>Date: 24-Feb-1994 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: E47758
R:Voyleas, D.F.; Cummings, M.P.; Konieczny, A.; Ausubel, F.M.; Rodermel, S.R.
Proc. Natl. Acad. Sci. U.S.A. 89, 7124-7128, 1992
A:Title: copia-like retrotransposons are ubiquitous among plants.
A:Reference number: A46200; MUID:92357784; PMID:1379734
A:Contents: clone 2
A:Accession: E47758
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-89 <VOY>
A:Cross-references: UNIPROT:Q06293; GB:M94478; NID:g439435; PIDN:AAA33403.1; PID:g168308
A>Note: sequence extracted from NCBI backbone (NCBIP:111898)
C:Superfamily: retrovirus-related polyprotein

Query Match 6.9%; Score 64.5; DB 2; Length 89;
Best Local Similarity 26.8%; Pred. No. 39;
Matches 26; Conservative 13; Mismatches 23; Indels 35; Gaps 5;

QY 86 GYEVQKVF-----LHLSMHGISQILQGFACMPHEHRDVSFCVLVSRGGSQSYGVVDQTH 139
Db 20 GYTVQGAENKVKLRSLRSLYGLKQLLKQW-----YKKFDSF---WMSRGFSKSEY----- 65

QY 140 SGLPLHHRMFMGDCPCPYLAG-KPKMFFIQTNYVSD 175
Db 66 -----DYCVVFETLNYEKFLISVPYVDD 88
```

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RESULT 9
T17929
hypothetical protein A426R - Chlorella virus PBCV-1
C:Species: Chlorella virus PBCV-1
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T17929
R:Graves, M.V.; Van Etten, J.L.
submitted to the EMBL Data Library, May 1999
A:Reference number: Z18806
A:Accession: T17929
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-114 <GRA>
A:Cross-references: UNIPROT:Q98478; EMBL:U42580; NID:g4028896; PIDN:AAC96794.1
A:Experimental source: specific host Chlorella strain NC64A
C:Genetics:
A>Note: A426R

Query Match 6.9%; Score 64.5; DB 2; Length 114;
Best Local Similarity 23.5%; Pred. No. 52;
Matches 23; Conservative 19; Mismatches 33; Indels 23; Gaps 3;

QY 4 VQAGTSYRNVLQAATQKSLKDPNSNNFREPEPVKKSQTQSEAFLPQSIPEERYKMKSKPLG 63
Db 1 MSEGHTVVERMLKVLVYRILE--ANSFRELLVPEKIKDTKKQIQP----- 43

QY 64 ICLIDICIGNETELLRTDFTTSIG---YEVQKFLHLSMH 98
Db 44 ---IIDMICSNYLNKDKFEQLNVDPVEIQNLQPLQNH 78

RESULT 10
H71267
conserved hypothetical protein TP0907 - syphilis spirochete
C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C>Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C:Accession: H71267
R:Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDo
rsey, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A:Reference number: A71250; MUID:98332770; PMID:9665876
A:Accession: H71267
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-174 <COL>
A:Cross-references: UNIPROT:O83877; GB:AE001259; GB:AE000520; NID:g3323209; PIDN:AAC6585
A:Experimental source: strain Nichols
C:Genetics:
A:Gene: TP0907

Query Match 6.9%; Score 64.5; DB 2; Length 174;
Best Local Similarity 31.6%; Pred. No. 89;
Matches 18; Conservative 11; Mismatches 19; Indels 9; Gaps 3;

QY 120 VCVLVSRGGSQSYGVVDQTHSG---LPLHHRMFMGDCPCPYLAGKPKMFFIQNYV 173
Db 123 VVLSVVEGGGSLLEVQRTHGVCVVPFH---RTFIGD---VDVGRKTIQLQRMIL 173

RESULT 11
S34363
hypothetical protein 18.3 - Salmonella typhimurium
C:Species: Salmonella typhimurium
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S34363
R:Persson, B.C.; Bjork, G.R.
submitted to the EMBL Data Library, June 1993
A:Description: Isolation of a gene (miaE) involved in hydroxylation of ms2106A in CRNA of
A:Reference number: S34359
A:Accession: S34363
A:Status: preliminary
```


Search completed: June 20, 2005, 13:44:48
Job time : 41 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2005, 13:33:55 ; Search time 175 Seconds
(without alignments)
517.932 Million cell updates/sec

Title: US-10-713-208-6_COPY_76_252

Perfect score: 930

Sequence: 1 KQSVQAGTSYRNVLQAIQ.....YLAGKPKMFFIQNVVSDGQ 177

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 571181

Minimum DB seq length: 0

Maximum DB seq length: 177

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_03.*

1: uniprot_prot.*

2: uniprot_trembl.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	277	29.8	78	Q8MJ18	Q8mj18 macaca mula
2	144	15.5	172	Q6PVY1	Q6pvy1 bos taurus
3	94.5	10.2	104	Q9UG96	Q9ug96 homo sapien
4	78.5	8.4	131	Q9CXM4	Q9cxm4 mus musculus
5	73.5	7.9	149	Q9Y056	Q9y056 caenorhabdi
6	72	7.7	176	YM04_VIEPA	Q87nm7 vibrio para
7	70.5	7.6	135	Q8YPR0	Q8ypr0 anabaena sp
8	69	7.4	152	Q97CY2	Q97cy2 clostridium
9	68.5	7.4	136	Q04355	Q04355 chlamydomon
10	68.5	7.4	159	Q6P7W6	Q6f7w6 acinetobact
11	68	7.3	89	Q93J15	Q93j15 streptomyc
12	68	7.3	137	LYC_BOMMO	P48816 bombyx mori
13	67.5	7.3	174	Q734A9	Q734a9 bacillus ce
14	67	7.2	125	Q669Y8	Q669y8 yersinia ps
15	67	7.2	125	Q8ZDW3	Q8zdw3 yersinia pe
16	66	7.1	96	Q9AXB5	Q9axb5 oryza sativ
17	66	7.1	133	Q7P252	Q7p252 chromobact
18	65.5	7.0	145	Q6ZZX9	Q6zzx9 platichthys
19	65.5	7.0	164	Q20267	Q20267 caenorhabdi
20	64.5	6.9	89	Q06293	Q06293 liroidendro
21	64.5	6.9	114	Q98478	Q98478 paramelicu
22	64.5	6.9	125	Q9DDM5	Q9ddm5 corytophane
23	64.5	6.9	135	Q9B581	Q9b581 lacerta viv
24	64.5	6.9	150	Q7SXI3	Q7sxi3 brachydanio
25	64.5	6.9	174	1 RIMM_TREPA	Q83877 treponema p
26	64	6.9	101	VE7_HPV21	P50779 human papil
27	64	6.9	119	Q9P816	Q9p816 issatchenki
28	64	6.9	135	Q9B579	Q9b579 lacerta viv
29	64	6.9	151	DKSA_BUCAP	Q8k9us buchnera ap
30	63.5	6.8	135	Q9BOR7	Q9bor7 lacerta viv
31	63.5	6.8	135	Q9BOR8	Q9bor8 lacerta viv

32	63.5	6.8	135	2	Q9B580	Q9b580 lacerta viv
33	63.5	6.8	135	2	Q9B583	Q9b583 lacerta viv
34	63.5	6.8	135	2	Q9B586	Q9b586 lacerta viv
35	63.5	6.8	153	1	Y9G4A0	Q894a0 clostridium
36	63.5	6.8	167	1	YJGM_SALTY	Q8021 salmonella
37	63.5	6.8	171	2	Q821Z0	Q82120 salmonella
38	63	6.8	132	2	Q6DNH3	Q6dnh3 uncultured
39	63	6.8	172	2	Q9KNU9	Q9knu9 vibrio chol
40	62.5	6.7	110	2	Q84SM2	Q84sm2 oryza sativ
41	62.5	6.7	119	2	Q6FVN0	Q6fvn0 candida gla
42	62.5	6.7	126	2	Q9NGQ9	Q9ngq9 tribolium c
43	62.5	6.7	127	2	Q79F17	Q79f17 enterococc
44	62.5	6.7	135	2	Q8LU47	Q8lu47 zootoca viv
45	62.5	6.7	135	2	Q9B1W8	Q9b1w8 lacerta viv

ALIGNMENTS

RESULT 1

Q8MJ18 PRELIMINARY; PRT; 78 AA.
 ID Q8MJ18;
 AC Q8MJ18;
 DT 01-OCT-2002 (Tremblrel. 22, Created)
 DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Flice/caspase-1 inhibitory protein (Fragment).
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
 OC Cercopitheidae; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Petit F., Arnould D., Lelievre J.-D., Lecossier D., Hance A.J.,
 RA Monceaux V., Ho Tsong Fang R., Hurtrel B., Ameisen J.-C.,
 RA Estaquier J.;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF530077; AAM95637.1;
 FT NON_TER 1
 FT NON_TER 78
 SQ SEQUENCE 78 AA; 8971 MW; 6BD208095731A99 CRC64;

Query Match 29.8%; Score 277; DB 2; Length 78;
 Best Local Similarity 73.1%; Pred. No. 6.4e-19;
 Matches 57; Conservative 2; Mismatches 1; Indels 18; Gaps 1;

QY 11 YRNVLGAAATKSLKDPNNFR-----EPPVKSIQSEAFPOSPE 52
 Db 1 YKNVLQAATQSLKDPNNFRLNHGRSKQRLKEQLGTQOEPVKTSIQSEAFPOSPE 60
 QY 53 ERYKMKSKPLGICLIIDC 70
 Db 61 ERYKMKSKPLGICLIIDC 78

RESULT 2

Q6PVY1 PRELIMINARY; PRT; 172 AA.
 ID Q6PVY1;
 AC Q6PVY1;
 DT 05-JUL-2004 (Tremblrel. 27, Created)
 DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
 DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
 DE Caspase-3 (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tao W., Mallard B., Karrow N., Bridle B.;
 RT "Construction and application of a bovine immune-endocrine cDNA

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RT microarray.";
RL Vet. Immunol. Immunopathol. 101:1-17(2004).
CC -I- SIMILARITY: Belongs to the peptidase C14 family.
DR EMBL; AY573000; RAS93968.1; -.
DR HSSP; P55210; IK86.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0008234; F:cysteine-type peptidase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR PRINTS; PR00376; IL1BCENZYM.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
KW Hydrolase; Protease; Thiol protease; Zymogen.
FT NON_TER 1
FT NON_TER 172
FT NON_TER 172
SQ SEQUENCE 172 AA; 19333 MW; 6CEB4E7920693A9D CRC64;

Query Match 15.5%; Score 144; DB 2; Length 172;
Best Local Similarity 31.1%; Pred. No. 1e-05;
Matches 38; Conservative 24; Mismatches 42; Indels 18; Gaps 5;

QY 62 LGICLIID-----C-IGNETEL--LRDTFTSLGYEQKFLHLSMHGISOILGQF 107
DB 3 MGLCIINNNKFNHENTGMACRSGTDVDAANLRETFMNLYEVRINKDLTKEMLELMSNV 62

QY 108 ACMPHERDYDSFVCVLVSRGGSQSVGVQDTHSGGLPLHHRIRMFMGDSCPYLAGKPKMFF 167
DB 63 S-KEDHSKSSPICVLLSGEGILFG---TNGPVNKKLASFFRGDYCRSLTGPKLFI 118

QY 168 IQ 169
DB 119 IQ 120

RESULT 3
Q9UG96 PRELIMINARY; PRT; 104 AA.
AC Q9UG96;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein DKFZp586A181 (Fragment).
GN Name=DKFZp586A181;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RA Wambutt R., Heubner D., Mewes H.W., Gassenhuber J., Wiemann S.;
RA Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL050391; CAB43686.2; -.
DR HSSP; P29466; 1ICE.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR PRINTS; PR00376; IL1BCENZYM.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
KW Hypothetical protein.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 104 AA; 11587 MW; 10411DF1306C1432 CRC64;
```

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Query Match 10.2%; Score 94.5; DB 2; Length 104;
Best Local Similarity 28.4%; Pred. No. 0.33;
Matches 27; Conservative 18; Mismatches 47; Indels 3; Gaps 2;

QY 78 LRDTFTSLGYEQKFLHLSMHGISOILGQFACMPEHRDYDSFVCVLVSRGGSQSVGV-- 135
DB 3 MKELLEGDYSDVVEENLTARDMESALRAFATRPEHKSSDSTFLVMSHGILGICGTVH 62

QY 136 DQTHSGGLPLHH-IRRMFMGSDSCPYLAGKPKMFFIQ 169
DB 63 DEKPDVLLYDTIPQIFNNRNCLSLKDKPKVLIIVQ 97

RESULT 4
Q9CXM4 PRELIMINARY; PRT; 131 AA.
ID Q9CXM4
AC Q9CXM4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mus musculus 13 days embryo head cDNA, RIKEN full-length enriched
DE library, clone:3110059017 product:caspase 3, apoptosis related
DE cysteine protease, full insert sequence.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RC MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RA "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RC MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RA "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RA The FANTOM Consortium;
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RC MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RC MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara S., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
```

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RC STRAIN=C57BL/6J; TISSUE=Head;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Hanakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK014231; BAB29219.1; -.
DR HSSP; P42574; INME.
DR GO; GO:0030693; F:caspace activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR PRINTS; PR00376; IL1BCENZME.
DR PROSITE; PS50208; CASPASE_P20; 1.
KW Peptidase.
SQ SEQUENCE 131 AA; 14799 MW; 2B36D12AC47F62C7 CRC64;

Query Match 8.4%; Score 78.5; DB 2; Length 131;
Best Local Similarity 27.5%; Pred. No. 15;
Matches 30; Conservative 19; Mismatches 37; Indels 23; Gaps 6;

QY 28 NNFREPPV--KKSIOESEAFLPOSIPERYKMSKPLGICLIID-----CIGN 73
DB 14 NNFVKTIGSKSV-DSGIYLDSS-----YKMDYPEMGICIIINNKNFKHSTGMSRSRG 67

QY 74 ETEL--LRDTFTSLGYEVQKFLHSMHGISQILGQFACMP-EHRDYDSF 119
DB 68 DVDAAANLRETFMGLKQVRKNKNDLTREDILELMDSGKIEPIQSRFGSF 116

RESULT 5
QY056 PRELIMINARY; PRT; 149 AA.
AC QY056;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Caspase-related protein 1C (Hypothetical protein Y48E1B.13c).
GN Name-csp-1; Synonyms=Y48E1B.13c; ORFNames=Y48E1B.13;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=N2;
RX MEDLINE=99074291; PubMed=9857046; DOI=10.1074/jbc.273.52.35109;
RA Shaham S.;
RT "Identification of multiple Caenorhabditis elegans caspases and their
RT identical roles in proteolytic cascades.";
RL J. Biol. Chem. 273.35109-35117 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C. elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018 (1998).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA McMurray A.A.;
RT Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF088287; AAC98294.1; -.
DR EMBL; Z93393; CAD18880.1; -.
DR FIR; T43637; T43637.
DR HSSP; P42575; IPYO.
DR WormBase; WBGene0000819; csp-1.
DR WormPeP; Y48E1B.13c; CE30017.
DR GO; GO:0030693; F:caspace activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR PRINTS; PR00376; IL1BCENZME.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS01121; CASPASE_HIS; UNKNOWN 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
KW Hypothetical protein.
SQ SEQUENCE 149 AA; 16921 MW; 0C5943D53DE16BC7 CRC64;

Query Match 7.9%; Score 73.5; DB 2; Length 149;
Best Local Similarity 28.7%; Pred. No. 53;
Matches 27; Conservative 16; Mismatches 36; Indels 15; Gaps 4;

QY 55 YMKSKPLGICLIID-----CIGNETELLRDT--FTSLGYEVQKFLHLSMHGISQI 103
DB 17 YEMNSNPRGTVLILSNENFKMMERRVGTQDEVNLTKLQKLYTVICKRNLEAESMLEA 76

QY 104 LQQFACMPEHRDYSFVCLVSRG-GSQSVYGV 136
DB 77 IKEFA---EMAHTDSIILFLSLSHGDGAGSVFGID 107

RESULT 6
YMO4_VIBPA STANDARD; PRT; 176 AA.
AC Q87MM7;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Hypothetical UPF0115 protein VP2204.
GN OrderedLocNames=VP2204;
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=670;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RIMD 2210633 / Serotype O3:K6;
RX MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
RT distinct from that of V. cholerae.";
RL Lancet 361:743-749 (2003).
CC -!- SIMILARITY: Belongs to the UPF0115 family.
CC -!- SIMILARITY: Contains 1 Smr domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
DR EMBL; AP005080; BAC60467.1; -.
DR HAMAP; MF_01042; -.
DR InterPro; IPR002625; Smr/MutS2_C.
DR Pfam; PF01713; Smr; 1.
DR SMART; SM00463; SMR; 1.
DR PROSITE; PS50828; SMR; 1.
KW Complete proteome; Hypothetical protein.
FT DOMAIN 97 172 Smr
SQ SEQUENCE 176 AA; 20200 MW; D6562D0E7D7EDC46 CRC64;
```

Query Match		7.7%;	Score 72;	DB 1;	Length 176;
Best Local Similarity		23.9%;	Pred. No. 90;		
Matches		37;	Conservative	31;	Mismatches 53; Indels 34; Gaps 9;
QY	1	KOSVQAGTSYRNVLQAAIQKSLKDPNNFREPVKKSIOE-----SEAFLOPSIPE	52		
DB	16	KEAVQGV-----KKLRDITI---IQPKNTKQKEIKRSNREASDSEFYPSDFVPLNBE	68		
QY	53	-----ERYKMSKPLGIC---LIIDCIG-NETELLRTFTSLGYEVQKFLHLS--	96		
DB	69	GPTRYARDVSYEVKRLRGVYVDVFLDMGTQOEAKRELGAIAVCVKNRHCACV	128		
QY	97	MHGISO-ILGQFA--CMPEHRDYDSVFCVVLVRGG	128		
DB	129	QHGHGKHLKQAPLQAHPDWMAPHQAPLEFGG	163		
RESULT 7					
Q8YPRO PRELIMINARY; PRT; 135 AA.					
ID	Q8YPRO;				
AC	Q8YPRO;				
DT	01-MAR-2002 (TrEMBLrel. 20, Created)				
DT	01-MAR-2002 (TrEMBLrel. 20, Last sequence update)				
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)				
DE	Alr4132 protein.				
GN	OrderedLocusNames=alr4132;				
OS	Anabaena sp. (strain PCC 7120).				
OC	Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.				
OX	NCBI_TaxID=103690;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	MEDLINE=21595285; PubMed=11759840;				
RA	Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,				
RA	Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,				
RA	Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,				
RA	Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,				
RA	Yasuda M., Tabata S.;				
RT	"Complete genomic sequence of the filamentous nitrogen-fixing				
RT	Cyanobacterium Anabaena sp. strain PCC 7120."				
RL	DNA Reg. 8:205-213(2001).				
DR	EMBL; AF003595; BAB75831.1; --				
DR	PIR; AE2322; AE2322.				
DR	HSSP; Q57997; 1MJH.				
DR	GO; GO:0006950; P:response to stress; IEA.				
DR	Pfam; PF00582; Usp; 1.				
DR	PRINTS; PR01439; UNVRSLSSTRESS.				
KW	Complete proteome.				
SQ	SEQUENCE 135 AA; 14442 MW; BF77512CB6FA6BC2 CRC64;				
Query Match		7.6%;	Score 70.5;	DB 2;	Length 135;
Best Local Similarity		33.8%;	Pred. No. 91;		
Matches		25;	Conservative	15;	Mismatches 27; Indels 7; Gaps 4;
QY	4	VQAGTSYRNVLQAAIQKSLKDPNN---NFREPVKKSIOSEA-FLPOSIPERYKMS	59		
DB	26	VQKYG--RLILSVVEESPDESSADPMWSPBAVKLLRDAQALFLOQGISIVEIKQG	83		
QY	60	KP-LGICLIIDCIG	72		
DB	84	KPAFTICDVADEIG	97		
RESULT 8					
Q97CY2 PRELIMINARY; PRT; 152 AA.					
ID	Q97CY2;				
AC	Q97CY2;				
DT	01-OCT-2001 (TrEMBLrel. 18, Created)				
DT	01-OCT-2001 (TrEMBLrel. 18, Last sequence update)				
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)				
DE	Hypothetical protein CAC3708.				
GN	OrderedLocusNames=CAC3708.				
OS	Clostridium acetobutylicum.				
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;					
Clostridium.					
OX	NCBI_TaxID=1488;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=ATCC 824 / DSM 792 / VKM B-1787;				
RX	MEDLINE=21359325; PubMed=11466286;				
RX	DOI=10.1128/JB.183.16.4823-4838.2001;				
RA	Noelling J., Breton G., Omselchenko M.V., Makarova K.S., Zeng Q.,				
RA	Gibson R., Lee H.M., Dubois J., Oiu D., Hitti J., Wolf Y.I.,				
RA	Tatusov R.L., Sabathe F., Doucette-Stamm L.A., Soucaille P.,				
RA	Daly M.J., Bennett G.N., Koonin E.V., Smith D.R.;				
RT	"Genome sequence and comparative analysis of the solvent-producing				
RT	bacterium Clostridium acetobutylicum."				
RL	J. Bacteriol. 183:4823-4838(2001).				
DR	EMBL; AE007866; AAK81628.1; --				
DR	PIR; A97355; A97355.				
KW	Complete proteome; Hypothetical protein.				
SQ	SEQUENCE 152 AA; 17127 MW; 24EB2335E1D66FED CRC64;				
Query Match		7.4%;	Score 69;	DB 2;	Length 152;
Best Local Similarity		28.9%;	Pred. No. 1.5e+02;		
Matches		22;	Conservative	16;	Mismatches 26; Indels 12; Gaps 2;
QY	19	IQKSLKDPNNFREPVKKSIOSEAFLPOSIPERYKMSKPLGICLIIDCIGNETELL	78		
DB	86	LKKALDAPTASKKEPVKPKIVETAMPKAEAEVKVPKSTP-----VKKEPENP	136		
QY	79	RDFTTSL---GYEVQK	91		
DB	137	YDPFYKLRKHGKEVKK	152		
RESULT 9					
O04355 PRELIMINARY; PRT; 136 AA.					
ID	O04355;				
AC	O04355;				
DT	01-JUL-1997 (TrEMBLrel. 04, Created)				
DT	01-JUL-1997 (TrEMBLrel. 04, Last sequence update)				
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)				
DE	M19,000 outer arm dynein light chain.				
OS	Chlamydomonas reinhardtii.				
OC	Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;				
OC	Chlamydomonadaceae; Chlamydomonas.				
OX	NCBI_TaxID=3055;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=1132D;				
RX	MEDLINE=97311077; PubMed=9166408; DOI=10.1083/jcb.137.5.1081;				
RA	Patel-King R.S., Benashski S.E., Harrison A., King S.M.;				
RT	"A Chlamydomonas homologue of the putative murine t complex distorter				
RT	Tctex-2 is an outer arm dynein light chain."				
RL	J. Cell Biol. 137:1081-1090(1997).				
DR	EMBL; U89649; AAB58383.1; --				
DR	PIR; T08216; T08216.				
DR	InterPro; IPR005334; Tctex.				
DR	Pfam; PF03645; Tctex-1; 1.				
SQ	SEQUENCE 136 AA; 15883 MW; A42D37012E91262A CRC64;				
Query Match		7.4%;	Score 68.5;	DB 2;	Length 136;
Best Local Similarity		22.6%;	Pred. No. 1.4e+02;		
Matches		26;	Conservative	28;	Mismatches 40; Indels 21; Gaps 5;
QY	6	GAGTSY-RNVLQAAIQKSLKDPNNFREPVK-----KSIOSEAFLPOSIPERYKM--	57		
DB	28	GPNTKFERHKVQAVLKQVLKRIEKQKYPVKGQIQSLQDLREKVALGYDKLVI	87		
QY	58	-----KSKPLGICLIIDCIGNETELLRTFTSLGYEVQKFLHLSMHGISQILGQF	107		
DB	88	QVTVGQKQGQAMRIISRLWDQT---NDNFASEYENE-----SMYCVQVVGLY	134		
RESULT 10					


```
Q6F7W6
ID Q6F7W6 PRELIMINARY; PRT; 159 AA.
AC Q6F7W6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=AC12AD3160;
OS Acinetobacter sp. (strain ADP1)
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=62977;
RN [1]
RP SEQUENCE FROM N.A.
RA Barbe V., Vallienet D., Fonknechten N., Kreimeyer A., Oztas S.,
RA Labarre L., Cruveiller S., Robert C., Duprat S., Wincker P.,
RA Ornston L.N., Weissenbach J., Marliere P., Cohen G.N., Medigue C.;
RT "Unique features revealed by the genome sequence of Acinetobacter sp.
RT ADP1, a versatile and naturally transformation competent bacterium.";
RL Nucleic Acids Res. 0:0-0(2004).
DR EMBL: CR543861; CAG69849.1; -.
DR InterPro: IPR020336; UPF0054.
DR Pfam: PF02130; UPF0054.1.
DR ProDom: PD005688; UPF0054.1.
DR TIGRFAMs: TIGR00043; UPF0054.1.
DR PROSITE: PS01306; UPF0054.1.
KW Complete proteome.
SQ SEQUENCE 159 AA; 17922 MW; ECCA1638997EE06D' CRC64;

Query Match
Best Local Similarity 7.4%; Score 68.5; DB 2; Length 159;
Matches 28; Conservative 23; Mismatches 30; Indels 53; Gaps 7;

QY 15 LQAIIQKSLKPSNNPESPVKSIQ-----ESEAFL----- 46
Db 3 LNLSLQAQFKSPDLAKRAHKAIETLHDHVEKTDSEIGIACVDHQSHRLNLEYRCK 62
QY 47 -----QPSIPERYK-MKSKPLG---ICL--IIDICGNETELLRTFTSLGVEYVK 91
Db 63 DKSTNVLPSPDIPESVPLLDLPGLDVLICIPVVLD-----EAIEQHKTAQAH---- 112
QY 92 FLHLSMHGHSQILG 105
Db 113 FHHMLVHGTLHLG 126

QY 93J15 PRELIMINARY; PRT; 89 AA.
AC Q93J15;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein SC03993.
GN ORFNames=SCBAC25E3.30c;
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RC MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neill S.,
RA Rabinowitch E., Rajandream M.A., Rutherford K.M., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces

QY 108 ACMP-----EHRDYSFVCLVSRGQS-QS-VYGVDTHTGSLPLHH-----IRMFMDGSCP 157
Db 26 ACLTSEYVSHRDAIFVNCU-----GPRQSRHYVYVNETHEGCPVHSARWPDVDMFVGNACC 81
QY 158 YLA 160
Db 82 VVA 84

Query Match
Best Local Similarity 7.3%; Score 68; DB 2; Length 89;
Matches 21; Conservative 11; Mismatches 17; Indels 14; Gaps 4;

QY 108 ACMP-----EHRDYSFVCLVSRGQS-QS-VYGVDTHTGSLPLHH-----IRMFMDGSCP 157
Db 26 ACLTSEYVSHRDAIFVNCU-----GPRQSRHYVYVNETHEGCPVHSARWPDVDMFVGNACC 81
QY 158 YLA 160
Db 82 VVA 84

RESULT 12
LYC_BOMMO STANDARD; PRT; 137 AA.
AC P48816; Q9TWL7;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Lysozyme precursor (EC 3.2.1.17) (1,4-beta-N-acetylmuramidase).
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fat body;
RC MEDLINE=95394356; PubMed=7665079; DOI=10.1016/0378-1119(95)00199-G;
RA Lee W.J., Brey P.T.;
RT "Isolation and characterization of the lysozyme-encoding gene from the
RT silkworm Bombyx mori.";
RL Gene 161:199-203(1995).
RN [2]
RP SEQUENCE OF 19-38, AND FUNCTION.
RC STRAIN=NB18; TISSUE=Larval hemolymph;
RC MEDLINE=95181849; PubMed=7876591; DOI=10.1006/jipa.1995.1003;
RA Abraham E.G., Nagareju J., Salunke D., Gupta H.M., Datta R.K.;
RT "Purification and partial characterization of an induced antibacterial
RT protein in the silkworm, Bombyx mori.";
RL J. Invertebr. Pathol. 65:17-24(1995).
CC -!- FUNCTION: Lysozymes have primarily a bacteriolytic function; those
CC in tissues and body fluids are associated with the monocyte-
CC macrophage system and enhance the activity of immunosagents. Active
CC against E.coli and M.luteus.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages between N-
CC acetyl-D-glucosamine and N-acetylmuramic acid in peptidoglycan
CC heteropolymers of the prokaryotes cell walls.
CC -!- DEVELOPMENTAL STAGE: Expressed within 6 hours after induction,
CC reaches maximum levels after 48 hours and declines after 72 hours
CC after induction.
CC -!- INDUCTION: By bacterial infection.
CC -!- SIMILARITY: Belongs to the glycosyl hydrolase 22 family.
CC
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CC
CC EMBL: L37416; AAB40947.1; -.
CC PIR: JC4233; JC4233.
CC PDB: 1GD6; X-ray; A=19-137.
CC InterPro: IPR001916; Glyco_hydro_22.
DR
```



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AC O8ZDW3;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative membrane protein.
GN OrderedLocusNames=YPO2435;
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_taxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CO-92 / Biovar Orientalis;
RX MEDLINE=21470413; PubMed=11596360; DOI=10.1038/35097083;
RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA Prentice M.B., Sebaihia M., James K.D., Churcher C.M., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.-M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.M.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrall B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague.";
RL Nature 413:523-527(2001).
DR EMBL; AJ414152; CAC91240.1; -.
DR PIR; AD0297; AD0297.
KW Complete proteome.
SQ SEQUENCE 125 AA; 14092 MW; 0C82AC4B3215289A CRC64;

Query Match          7.2%; Score 67; DB 2; Length 125;
Best Local Similarity 25.0%; Pred. No. 1.8e+02;
Matches 17; Conservative 10; Mismatches 15; Indels 26; Gaps 2;

QY 86 GYEVQKFLHLSMHGIGSILGQFACMPE-----HRDYDSFV-----120
DB 26 GYQLAKFIRVVMHSGQAIDKKSLPRTDPAPHRVYISFVNVHNSAKNDLHYRLLLSSA 85
QY 121 -CVLVSRG 127
DB 86 GCIAISTG 93

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Search completed: June 20, 2005, 13:44:04
 Job time : 177 secs

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OM protein - protein search, using sw model

Run on: June 20, 2005, 13:30:56 ; Search time 160 Seconds
(without alignments)
427.854 Million cell updates/sec

Title: US-10-713-208-6_COPY_76_252

Perfect score: 930

Sequence: 1 KQSVQAGSYRNLQAIIQ.....YLAGKPKFFIYVVDGQ 177

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 1389662

Minimum DB seq length: 0
Maximum DB seq length: 177

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001s:*
- 5: Geneseq2002s:*
- 6: Geneseq2003as:*
- 7: Geneseq2003bs:*
- 8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	325	34.9	175	2 AAY05794	MRIT-D/S
2	166	17.8	147	7 ADL18190	Human cas
3	166	17.8	147	8 ADP20044	Human cas
4	154	16.6	167	4 AAM31155	Peptide #
5	130	14.0	163	4 AAM68529	Human bon
6	130	14.0	163	5 ABG38107	Human pep
7	108	11.6	158	5 AAE16024	Human cas
8	102	11.0	125	4 AAO02627	Human pol
9	78	8.4	146	8 ADO63844	Human 213
10	73	7.8	39	3 AAB14254	Partial m
11	71.5	7.7	101	6 ADA41128	Human sec
12	71.5	7.7	101	6 ABR47936	Human sec
13	71.5	7.7	101	6 ABR00176	Human gen
14	71.5	7.7	101	7 ADB91676	Human sec
15	71.5	7.7	101	7 ADC74344	Human sec
16	71.5	7.7	102	2 AAY41346	Human sec
17	70.5	7.6	173	8 ADL05651	M. catarr
18	67.5	7.3	133	6 ADB07674	Alloioioc
19	66.5	7.2	102	5 ABR31818	Human ORF
20	66.5	7.2	169	5 ABP51964	Helicobac
21	66	7.1	167	8 ADO43472	B. subtil
22	65	7.0	100	6 ABP60619	Human zin
23	65	7.0	117	2 AAY12157	Human 5'
24	64.5	6.9	174	6 ABU48709	Protein e
25	64	6.9	130	6 ABM5939	Protein b

ALIGNMENTS

RESULT 1

AAY05794
ID AAY05794 standard; protein; 175 AA.

XX AAY05794;

XX AC AAY05794;

DT 02-AUG-1999 (first entry)

XX XX

DE MRIT-D/S polypeptide.

XX KW MRIT-D/S; MACH related inducer of toxicity; human; apoptosis;

XX KW anti-apoptotic; cancer; autoimmune disease; angiogenesis;

XX KW atherosclerosis; neurodegenerative disease; Alzheimer's disease;

XX KW Parkinson's disease; retinitis pigmentosa; stroke; AIDS; infection;

XX KW aplastic anaemia; myocardial infarction; therapy; mutant.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO9918230-A2.

XX PD 15-APR-1999.

XX PF 07-OCT-1998; 98WO-US021132.

XX PR 07-OCT-1997; 97US-00946226.

XX PA (UNIW) UNIV WASHINGTON.

XX PI Chaudhary PM;

XX DR WPI; 1999-277275/23.

XX PS Identifying regulators of MACH-related inducer of toxicity.

XX PS Example 2; Page; 78pp; English.

XX CC

XX CC

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XX CC

CC the MRIT alpha 1 sequence given in figure 1F
XX Sequence 175 AA;
SQ
Query Match 34.9%; Score 325; DB 2; Length 175;
Best Local Similarity 98.4%; Pred. No. 2.5e-30;
Matches 60; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 117 DSFVCLVSRGGSQSYGVVDQTHSGPLPLHHRMFMDSCPYLAGKPKMFFIQNVVSDG 176
DB 1 DSFVCLVSRGGSQSYGVVDQTHSGPLPLHHRMFMDSCPYLAGKPKMFFIQNVVSEG 60
QY 177 Q 177
DB 61 Q 61
RESULT 2
ID ADL18190 standard; protein; 147 AA.
AC ADL18190;
XX
XX 06-MAY-2004 (first entry)
DT Human caspase 3 large subunit SEQ ID NO:110.
DE
DE chimeric protein; signal protein; trafficking signal targeting;
KW proteolytic cleavage site; protease; protease inhibitor; enzyme; human;
KW caspase 3.
OS Homo sapiens.
XX
XX WO2003014381-A1.
PN
XX
XX 20-FEB-2003.
XX
XX 08-AUG-2002; 2002WO-KR001515.
PF
XX
XX 10-AUG-2001; 2001KR-00048123.
PR
XX
XX (AHRA-) AHRAM BIOSYSTEMS INC.
PA
XX
XX Hwang I, Kim DH, Lee YJ;
PI
XX
XX WPI; 2003-256596/25.
DR
XX
XX N-PSDB; ADL18189.
DR
XX
XX New chimeric protein, useful for detecting protease inhibitors inside the
PT cell or tissue.
XX
XX Disclosure; SEQ ID NO 110; 214pp; English.
XX
XX The present invention describes a chimeric protein comprising at least
CC one signal protein that has a trafficking signal targeting to a
CC subcellular organelle and at least one proteolytic cleavage site for a
CC protease. The chimeric protein is constructed, so that: (a) the
CC trafficking signals of all the signal proteins are inactivated by linking
CC the proteolytic site or a signal masking protein through the proteolytic
CC site to the N- or C- terminus of the signal proteins, and so the chimeric
CC protein is present in cytosol; (b) the trafficking signal of at least one
CC signal protein is activated when the proteolytic cleavage site is cleaved
CC by the protease, and as a result at least one fragment protein that
CC includes the activated signal protein is transported to a subcellular
CC organelle; and (c) the chimeric protein is labelled with at least one
CC fluorescent protein and the position and intensity distribution of the
CC fluorescent label signal in the cell is altered depending on the cleavage
CC by the protease. Also described: (1) a recombinant gene comprising a
CC nucleic acid sequence encoding the chimeric protein which is constructed
CC to express the chimeric protein in a cell; (2) a cell transformed with
CC the recombinant gene or vector; (3) analysing the activity of a protease
CC in vivo; (4) screening protease inhibitors in vivo; (5) a system for
CC detecting a protease inside a cell; (6) a nucleic acid comprising the

CC sequence encoding the chimeric protein for detecting protease activity in
CC a cell; (7) a vector comprising the nucleic acid; (8) a kit for detecting
CC a protease inside a cell comprising the chimeric protein or the vector;
CC (9) detecting a protease inside a cell or tissue; and (10) detecting a
CC protease inhibitor in vivo. The chimeric protein is useful for detecting
CC protease inhibitors inside the cell or tissue. The present sequence
CC represents a human caspase 3 large subunit, which is used in the
CC exemplification of the present invention.
XX
XX Sequence 147 AA;
SQ
Query Match 17.8%; Score 166; DB 7; Length 147;
Best Local Similarity 32.6%; Pred. No. 3e-11;
Matches 43; Conservative 22; Mismatches 49; Indels 18; Gaps 4;
QY 52 EERYKMSKPLGICLIID-----CIGNETEL--LRDTFTSLGYEVQKFLHLSM 97
DB 6 DNSYKMDYPENGLCTIINNKNFKHSTGMTSRSRGTDVAANLRETPRNLUKEYVRNKNQDTR 65
QY 98 HGISOILGQFACMPPEHRDYSFVCLVSRGGSQSYGVVDQTHSGPLPLHHRMFMDGSCP 157
DB 66 EEIVELMRDVS-KEDHKSRSFVCLVLSHGEGIFG---TNGPVDLKKITNPFGRDCR 121
QY 158 YLAGKPKMFFIQ 169
DB 122 SLTGKPKLFIQ 133
QY
DB
RESULT 3
ADP20044
ID ADP20044 standard; protein; 147 AA.
XX
XX ADP20044;
AC
XX
XX 09-SEP-2004 (first entry)
DT
XX
XX Human caspase-3 mature protein SEQ ID NO:9.
DE
XX
XX human; caspase-3; stem cell differentiation; muscular dystrophy;
KW cardiovascular disease; stroke; heart failure; myocardial infarction;
KW neurodegenerative disease; neurodegenerative disorder;
KW degenerative liver disease; diabetes.
XX
XX Homo sapiens.
XX
XX WO2004053144-A2.
PN
XX
XX 24-JUN-2004.
PD
XX
XX 10-DEC-2003; 2003WO-CA001911.
PF
XX
XX 10-DEC-2002; 2002US-0431990P.
PR
XX
XX 10-DEC-2002; 2002US-0431991P.
PR
XX
XX (OTTA-) OTTAWA HEALTH RES INST.
PA
XX
XX Megeney L;
PI
XX
XX WPI; 2004-468878/44.
DR
XX
XX Screening for compounds that modulate stem cell differentiation comprises
PT identifying a modulator of caspase-3 activity by contacting a caspase-3
PT protein, or a cell expressing a caspase-3 protein, with a candidate
PT compound.
XX
XX Disclosure; SEQ ID NO 9; 108pp; English.
XX
XX The invention relates to a novel method for screening for compounds that
CC modulate stem cell differentiation comprising identifying a modulator of
CC caspase-3 activity by contacting a caspase-3 protein, or a cell
CC expressing a caspase-3 protein, with a candidate compound, measuring the
CC activity of the caspase-3 protein and comparing the measured activity
CC with the activity of caspase-3 protein in the absence of the candidate

CC compound. The methods of the invention are useful for screening for
CC compounds that modulate stem cell differentiation, where one or more
CC compound modulates caspase-3 activity by inhibiting or activating one
CC more component of the caspase-3 signaling pathway. A compound identified
CC by the methods of the invention is useful in the treatment of muscular
CC dystrophy, cardiovascular disease, stroke, heart failure, myocardial
CC infarction, neurodegenerative diseases/disorders, degenerative liver
CC diseases, and diabetes. The present sequence represents one form of
CC active caspase-3 protein.
XX
XX Sequence 147 AA;

Query Match	17.8%;	Score 166;	DB 8;	Length 147;
Best Local Similarity	32.6%;	Pred. No. 3e-11;		
Matches	43;	Conservative 22;	Mismatches 49;	Indels 18; Gaps 4;
Qy	52	BERYKMSKPLGICLIID-----CIGNETEL--LRDFTSISGEVQKFLHLSM	97	
Db	6	DSNYKMDYPENGLCIIINNNFKHSTGWTSRSGTDVDAANLRTEFRNLKTYEVRNKDLTR	65	
Qy	98	HGISIIQLQACMPEDHRDYDSFVCLVLSRGGSSQSYGVQDTHSGLPFLHIRRMFMGSDSCP	157	
Db	66	BEIVELMRDVS-KEDHKSRSFVCVLLSHGEEGIFG--TNGPVDLKKITNFRGRDRCR	121	
Qy	158	YLAKPKPMFFIQ	169	
Db	122	SLTGKPKLFIQ	133	

RESULT 4
AAM31155
ID AAM31155 standard; protein; 167 AA.
XX
XX
AC AAM31155;
XX
DT 17-OCT-2001 (first entry)
XX
DE Peptide #5192 encoded by probe for measuring placental gene expression.
XX
XX
KW Probe; microarray; human; placenta; antenatal diagnosis;
KW genetic disorder.
XX
OS Homo sapiens.
XX
XX
PN WO200157272-A2.
XX
XX
PD 09-AUG-2001.

XX	30-JAN-2001; 2001WO-US000663.
PF	
XX	
XX	04-FEB-2000; 2000US-0180312P.
PR	26-MAY-2000; 2000US-0207456P.
PR	30-JUN-2000; 2000US-00608408.
PR	03-AUG-2000; 2000US-00632366.
PR	21-SEP-2000; 2000US-0234687P.
PR	27-SEP-2000; 2000US-0236359P.
PR	04-OCT-2000; 2000GB-00024263.
XX	
PA	(NOLE-) MOLECULAR DYNAMICS INC.
XX	
PI	Penn SG, Hanzel DK, Chen W, Rank DR;
XX	
XX	WPI; 2001-488897/53.
DR	

XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human placenta.
XX
XX Claim 27; SEQ ID NO 31424; 654pp; English.
XX
XX The present invention relates to single exon nucleic acid probes (SENP: CC
CC see AA13135-AA157546). The present sequence is a peptide encoded by one CC
CC such probe. The probes are useful for producing a microarray for CC
CC predicting, measuring and displaying gene expression in samples derived CC
CC

CC	from human placenta. The probes are useful for antenatal diagnosis of
CC	human genetic disorders
XX	
SQ	Sequence 167 AA;
	Query Match 16.6%; Score 154; DB 4; Length 167;
	Best Local Similarity 35.4%; Pred. No. le-09;
	Matches 35; Conservative 18; Mismatches 38; Indels 8; Gaps 3
Qy	78 LRDFTSLGYEVOKFLHLSMHGTSIIIGQFACMPEHRDYSFVCLVSRGGSQSVMGVDDQ 137 : :
Dd	2 LTTTFEELHEFIKPHDDCTVEIQVEILKIQLM-DHSNMDCFCICILSHGDGIYGTGD 60
Qy	138 THSGLPLUHHTRRMFGSDSCPYLACKPKMFIIQ-----NY 171 : :
Dd	61 OEA--PIVELTSTOPTGLKCPSLAGKPVFVFIAOCQGDNY 97 :

RESULT 5
AAM68529
ID AAM68529 standard; protein; 163 AA.

XX	06-NOV-2001	(first entry)	Human bone marrow expressed probe encoded protein SEQ ID NO: 28835
DT			
DE			
XX			
XX			Human; bone marrow expressed exon; gene expression analysis; probe
KW			microarray; Cancer; leukaemia; lymphoma; myeloma.

OS	Homo sapiens.	
XX		
PN	WO200157276-A2.	
XX		
PD	09-AUG-2001.	
XX		
PF	30-JAN-2001; 2001WO-USO00668.	
XX		
PR	04-FEB-2000; 2000US-0180312P.	
PR	26-MAY-2000; 2000US-0207456P.	
PR	30-JUN-2000; 2000US-0060840B.	
PR	03-AUG-2000; 2000US-00632366.	
PR	21-SEP-2000; 2000US-0234687P.	
PR	27-SEP-2000; 2000US-0236359P.	
PR	04-OCT-2000; 2000GB-00024263.	
XX		
PA	(WO/01) MOLECULAR DYNAMICS INC.	

XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI
XX WPI: 2001-488900/53.

WPI; 2001-488900/53.

Example 4: SEO ID NO 28835: 658pp + Sequence Listing: English: PS

The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention

Sequence 163 AA;

Query Match 14.0%; Score 130; DB 4; Length 163;
Best Local Similarity 33.3%; Pred. No. 7.7e-07;
Matches 31; Conservative 17; Mismatches 43. Indels

QY 77 LLRDTFTSLGVEVQKFLHLSMHGISQILGQFACMPEHRDYSFVCVLVSRGGSQSVYGV 136

Db 1 ILSHVFQWLGFTVHHNNVTKMEMVQLQKQCNPAHADGDCVFVFCILTHGRFGAVYSSD 60

QY 137 QTHSGPLPHHRRMFMGDCPYLAGPKPMFFIQ 169

Db 61 E--ALIPREIMSHFTALQCPLAEKPKLFFIQ 91

RESULT 6

ABG38107

ID ABG38107 standard; peptide; 163 AA.

XX ABG38107;

AC ABG38107;

XX

DT 19-AUG-2002 (first entry)

XX

DE Human peptide encoded by genome-derived single exon probe SEQ ID 27772.

XX

KW Human; single exon probe; asthma; lung cancer; COPD; ILD;

KW chronic obstructive pulmonary disease; interstitial lung disease;

KW familial idiopathic pulmonary fibrosis; neurofibromatosis;

KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;

KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;

KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karsenger syndrome;

KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;

KW primary ciliary dyskinesia; pulmonary hypertension;

KW hyaline membrane disease.

XX

OS Homo sapiens.

XX

PN WO200186003-A2.

XX

PD 15-NOV-2001.

XX

PF 30-JAN-2001; 2001WO-US000665.

XX

PR 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX

PA (MOLE-) MOLECULAR DYNAMICS INC.

XX

PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX

DR WPI; 2002-114183/15.

XX

PT Spatially-addressable set of single exon nucleic acid probes, used to

PT measure gene expression in human lung samples.

XX

PS Claim 27; SEQ ID NO 27772; 634pp; English.

XX

CC The invention relates to a spatially-addressable set of single exon

CC nucleic acid probes for measuring gene expression in a sample derived

CC from human lung comprising single exon nucleic acid probes having one of

CC 12614 nucleic acid sequences mentioned in the specification, or their

CC complements or the 12387 open reading frames derived from the 12614

CC probes. Also included are a microarray comprising the novel set of probes

CC ; the novel set of probes which hybridise at high stringency to a nucleic

CC acid expressed in the human lung; measuring gene expression in a sample

CC derived from human lung, comprising (a) contacting the array with a

CC collection of detectably labeled nucleic acids derived from human lung

CC mRNA, and (b) measuring the label detectably bound to each probe of the

CC array; identifying exons in a eukaryotic genome, comprising (a)

CC algorithmically predicting at least one exon from genomic sequences of

CC the eukaryote; and (b) detecting specific hybridisation of detectably

CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,

CC having a fragment identical to the predicted exon, the probe is included

CC in the above mentioned microarray; assigning exons to a single gene,

CC comprising (a) identifying exons from genomic sequence by the method

CC above and (b) measuring the expression of each of the exons in several

CC tissues and/or cell types using hybridisation to a single exon

CC microarrays having a probe with the exon, where a common pattern of

CC expression of the exons in the tissues and/or cell types indicates that

CC the exons should be assigned to a single gene; a peptide comprising one

CC of 12011 sequences, mentioned in the specification, or encoded by the

CC probes/open reading frames (ORF). The probes are used for gene expression

CC analysis, and for identifying exons in a gene, particularly using human

CC lung derived mRNA and for the study of lung diseases such as asthma, lung

CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung

CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,

CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-

CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary

CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,

CC Karsenger syndrome, fibrocystic pulmonary dysplasia, primary ciliary

CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The

CC present sequence is a peptide/protein encoded by a single exon probe of

CC the invention. Note: The sequence data for this patent did not form part

CC of the printed specification, but was obtained in electronic format

CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX

XX Sequence 163 AA;

Query Match 14.0%; Score 130; DB 5; Length 163;

Best Local Similarity 33.3%; Pred. No. 7.7e-07;

Matches 31; Conservative 17; Mismatches 43; Indels 2; Gaps 1;

QY 77 LLRDTFTSLGVEQVKFLHLSMHGISQLGQFACMPHRRDYSFVCLVSRGGSQSVYGV 136

Db 1 ILSHVFQWLGFTVHHNNVTKMEMVQLQKQCNPAHADGDCVFVFCILTHGRFGAVYSSD 60

QY 137 QTHSGPLPHHRRMFMGDCPYLAGPKPMFFIQ 169

Db 61 E--ALIPREIMSHFTALQCPLAEKPKLFFIQ 91

RESULT 7

AAE16024

ID AAE16024 standard; protein; 158 AA.

XX

AC AAE16024;

XX

DT 26-MAR-2002 (first entry)

XX

DE Human caspase-12 isoform, KW-F protein.

XX

KW Human; cysteine-dependent aspartate-specific proteases; caspase-12; KW-F;

KW Parkinson's disease; ulcerative colitis; cytostatic; glomerulonephritis;

KW inflammatory bowel disease; hypersensitivity; rheumatoid arthritis; ALS;

KW amyotrophic lateral sclerosis; bronchitis; inflammatory; cardiovascular;

KW neurodegenerative disease; Crohn's disease; Alzheimer's disease; cancer;

KW allergic rhinitis; cell proliferative disorder; asthma.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Misc-difference 40

FT /note= "Encoded by TC"

FT Misc-difference 63. .64

FT /note= "Encoded by ATGTGAGAT"

XX

PN WO200185961-A2.

XX

PD 15-NOV-2001.

XX

PF 08-MAY-2001; 2001WO-US015103.

XX

PR 09-MAY-2000; 2000US-0203162P.

XX

PA (PHAA) PHARMACIA & UPJOHN.

XX

PI Kletzien RF, Reardon IM, Weiland KL;

XX

DR WPI; 2002-082900/11.

DR N-PSDB; AAD26259.
XX New human caspase-12 polynucleotides and polypeptides, useful for
PT screening modulators of caspase activity, e.g. inhibitors, especially for
PT treating e.g. inflammatory, cardiovascular or neurodegenerative diseases,
PT or cancer.
XX
XX
PS Claim 1; Page 172; 207pp; English.
XX
XX The invention relates to purified, isolated caspase-12 polypeptides and
CC their polynucleotides. Cysteine-dependent aspartate-specific proteases.
CC (caspases) are a family of proteases that cleave their substrates at
CC aspartic acid-X bonds. They are highly specific endopeptidases that
CC catalyze limited proteolysis. Caspase-12 polypeptides are useful for
CC screening modulators of caspase activity. Caspase-12 inhibitors are useful
CC for preventing or treating disorders involving inappropriate apoptosis,
CC cardiovascular diseases, neurodegenerative disorders (Alzheimer's disease,
CC Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis
CC (ALS)); inflammatory diseases (systemic inflammatory conditions and
CC conditions associated locally with migration and attraction of monocytes,
CC leukocytes and/or neutrophils); autoimmune diseases (rheumatoid or
CC reactive arthritis, acute glomerulonephritis, chronic glomerulonephritis,
CC inflammatory bowel diseases such as Crohn's disease, ulcerative colitis
CC and necrotizing enterocolitis); allergic reactions (allergic asthma,
CC chronic bronchitis, acute and delayed hypersensitivity, allergic rhinitis
CC and cell proliferative disorder (cancer). Cancers that may be treated
CC comprise lymphomas, carcinomas or hormone-dependent tumours. The present
CC sequence is human caspase-12 isoform, KW-F protein
XX
SQ Sequence 158 AA;
Query Match 11.6%; Score 108; DB 5; Length 158;
Best Local Similarity 26.4%; Pred. No. 0.00033;
Matches 42; Conservative 19; Mismatches 70; Indels 28; Gaps 4;
QY 26 PSNNFPEPVKKSIOESSEAFLOPSIPEERYKMSKPLGICLIIDC-----IGNE 74
Db 11 PHAHFELTKTKR-----DEYPVMEKERRCTCLAINRKKNFVYLNHNGSE 57
QY 75 TELL-RDTFTSLGYEVQKFLHLSMHGISQILGQFACMPHEHDYDSFVCVLSVSGSQSVY 133
Db 58 LDLIGMDLLENLGYSVVIKESLTAQEMETALRQFAAHPHQSSDSTFLVFMHSHILNGIC 117
QY 134 GV--DQTHSGLPLHHRFMGDCSPYLAGKPMFFIQ 169
Db 118 GTKHWQEPDVLHDDTIFEIFNNRNQCSLKDKEKVIIMQ 156
RESULT 8
AAO02627
ID AAO02627 standard; protein; 125 AA.
XX
AC AAO02627;
XX
DT AAO02627;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 16519.
XX
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation.
XX
OS Homo sapiens.
XX
XX WO200164835-A2.
XX
PD 07-SEP-2001.
XX
XX 26-FEB-2001; 2001WO-US0004927.
XX
XX 28-FEB-2000; 2000US-00515126.
PR 18-MAY-2000; 2000US-00577409.
(HYSE-) HYSEQ INC.
Tang YT, Liu C, Drmanac RT;
WPI; 2001-514838/56.
N-PSDB; AAI82558.
Isolated nucleic acids and polypeptides, useful for preventing diagnosing
and treating e.g. leukemia, inflammation and immune disorders.
Claim 20; SEQ ID NO 16519; 1399pp + Sequence Listing; English.
The invention relates to human polynucleotides (AAI79941-AAI93841) and
the encoded proteins (AAO00010-AAO13910) that exhibit activity relating to
cytokine, cell proliferation or cell differentiation or which may induce
production of other cytokines in other cell populations. The
polynucleotides and polypeptides are useful in gene therapy, vaccines or
peptide therapy. The polypeptides have various cytokine-like activities,
e.g. stem cell growth factor activity, haematopoiesis regulating
activity, tissue growth factor activity, immunomodulatory activity and
activity/inhibin activity and may be useful in the diagnosis and/or
treatment of cancer, leukaemia, nervous system disorders, arthritis and
inflammation. Note: The sequence data for this patent did not form part
of the printed specification, but was obtained in electronic format
directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
Sequence 125 AA;
Query Match 11.0%; Score 102; DB 4; Length 125;
Best Local Similarity 24.4%; Pred. No. 0.0013;
Matches 32; Conservative 20; Mismatches 45; Indels 34; Gaps 4;
QY 17 AAIQKSLKDPNNFPEPVKKSIGSI---QSEAFLOPSIPEERYKMSKPLGICLIIDCIG 72
Db 6 ALYXRELFDPADKDKMDHSRGLVFNHFRFHWLSLPERR-----CTC 50
QY 73 NETELLRDTFTSLGYEVQKFLHLSMHGISQILGQFACMPHEHDYDSFVCVLSV 125
Db 51 SDRDNLNTRFSDLGFGKGFNDLKABELLLKHEVSTVI-----HSDADCFVCVFLS 102
QY 126 RGSQSQSVGVGD 136
Db 103 HGERNHVAYD 113
RESULT 9
ADO63844
ID ADO63844 standard; protein; 146 AA.
XX
AC ADO63844;
XX
DT 15-JUL-2004 (first entry)
XX
DE Human 213PIF11 variant 3.
XX
XX cytostatic; gene therapy; 213PIF11; 213PIF11 modulation; cancer;
KW transgenic; cytotoxic agent delivery; diagnostic agent delivery;
KW immune response; pancreatic cancer; rectal cancer; bladder cancer.
XX
OS Homo sapiens.
XX
XX US2004019915-A1.
XX
PD 29-JAN-2004.
XX
XX 01-APR-2002; 2002US-00114432.
XX
XX 01-APR-2002; 2002US-00114432.
XX
XX (CHAL/) CHALLITA-EID P M.
PA (RAIT/) RAITANO A B.
PA (FARI/) FARIS M.

PA (HUBE/) HUBERT R S.
PA (MORR/) MORRISON R K.
PA (GEWW/) GE W.
PA (JAKO/) JAKOBOVITS A.
XX
XX
PI Challita-Eid PM, Raitano AB, Faris M, Hubert RS, Morrison RK;
PI Ge W, Jakobovits A;
XX
DR N-PSDB; ADO63843.
XX
XX
PT New composition comprising a substance that modulates the status of
PT 213P1F11, or a molecule that is modulated by 213P1F11, useful for
PT detecting or treating cancer, e.g. pancreatic or rectal cancer.
XX
XX
PS Example 1; Fig 2; 334pp; English.
XX
CC The invention describes a composition comprising a substance that
CC modulates the status of 213P1F11, or a molecule that is modulated by
CC 213P1F11, where the status of the cell that expresses 213P1F11 is
CC modulated and 213P1F11 is a gene overexpressed in many cancers. Also
CC described are: a pharmaceutical composition comprising the composition
CC cited above in a unit dose form; an antibody or its fragment; a non-human
CC transgenic animal that produced the antibody; a hybridoma that produces
CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the
CC cell that expresses 213P1F11; a polynucleotide that encodes the protein;
CC inhibiting growth of cancer cells that expresses 213P1F11; generating a
CC mammalian immune response; detecting the presence of 213P1F11-related
CC protein or polynucleotide in a sample; and detecting the presence of
CC cancer in an individual. The compositions, molecules and methods are
CC useful for detecting and treating cancer, e.g. pancreatic or rectal
CC cancer. This is the amino acid sequence of human 213P1F11 gene variant 3.
XX
XX Sequence 146 AA;

Query Match 8.4%; Score 78; DB 8; Length 146;
Best Local Similarity 25.6%; Pred. NO. 1.2;
Matches 34; Conservative 22; Mismatches 61; Indels 16; Gaps 6;
QY 47 POSIPEERYKMSKPLGICLIIDCI-----GNETEL--LRDTFTSLGYEVQKFLHLSMHG 99
Db 4 PRSLEEEKYDMGARLALIL-:::--CVTKAREGSEEDLDAEHFRQRLRFSTWKRDPATAQ 60
QY 100 ISQILQFACMPEHRDYDSFVC---VLVSRGGSQSVYGVQDTHSGLPLHHIRRMFGDSC 156
Db 61 FQEELEKFOQADSRE-DPVSCAFVYLMAHREGFLKGED--GEMVYKLENLFEALNNKNC 117
QY 157 PYLAGPKPMFFIQ 169
Db 118 QALRAKPKVYIIQ 130

RESULT 10
AAB14254
ID AAB14254 standard; protein; 39 AA.

XX
AC AAB14254;
XX
DT 09-FEB-2001 (first entry)
DE Partial mouse nedd-2 protein #1.
XX
KW ced-3; virally induced cell death; apoptosis; gene therapy; neural;
KW muscular degenerative disease; myocardial infarction; stroke; aging;
KW interleukin-1beta converting enzyme; ICE; mouse; Ice-ced 3 homologue;
KW Ich; nedd-2.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT Domain 26..32
FT /label= Activa_domain
XX

PN US6083735-A.
XX
PD 04-JUL-2000.
XX
PF 10-JUN-1994; 94US-00258287.
XX
PR 24-JUN-1993; 93US-00080850.
XX
PA (GEO) GEN HOSPITAL CORP.
XX
PI Yuan J, Miura M;
XX
DR WPI; 2000-464343/40.
DR N-PSDB; AAA72837.
XX
PT New human Ich-1L and Ich-1S proteins for negative and positive regulation
PT of programmed cell death and for developing therapeutic methods for
PT diseases and conditions characterized by cell death, e.g. myocardial
PT infarction or stroke.
XX
PS Disclosure; Fig 9; 121pp; English.
XX
CC The present sequence is a partial mouse nedd-2 protein. Three possible
CC reading frames were deduced for the coding sequence of the present
CC protein. The first reading frame encodes the present protein, which has a
CC potential QACRG active domain. Nedd-2 is a member of a family of genes
CC involved in programmed cell death (apoptosis). Other family members
CC include: the ced-3 gene of C. elegans (AAA72802), human interleukin-1beta
CC converting enzyme (ICE) (AAB14250), murine ICE1 (AAB14249), human Ich-1
CC and murine ICE2 (AAB14252). Ich-1 may play an important role in both the
CC positive and negative regulation of apoptosis. The Ich gene may be used
CC in gene therapy in disorders characterised by cell death e.g. neural and
CC muscular degenerative diseases, myocardial infarction, stroke, virally
CC induced cell death and aging
XX
SQ Sequence 39 AA;
Query Match 7.8%; Score 73; DB 3; Length 39;
Best Local Similarity 53.8%; Pred. No. 0.72;
Matches 14; Conservative 3; Mismatches 9; Indels 0; Gaps 0;
QY 144 LHIRRMFGDSCPYLAGPKPMFFIQ 169
Db 3 LOEVFRLEDNANCPSLQNKPKMFFIQ 28
RESULT 11
ADA41128
ID ADA41128 standard; protein; 101 AA.
XX
AC ADA41128;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human secreted protein.
XX
KW Human; secreted protein; cancer; hyperproliferative disorder;
KW rheumatoid arthritis; autoimmune disorder; haematopoietic disorder;
KW anaemia; allergic reaction; asthma; cardiovascular disorder;
KW wound healing; cytostatic; immunosuppressive; neutrotropic; neuroprotective;
KW antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory;
KW vulneryary; cardiant; gene therapy.
XX
OS Homo sapiens.
XX
PN WO2002102993-A2.
XX
PD 27-DEC-2002.
XX
PF 19-MAR-2002; 2002WO-US008123.
XX
PR 21-MAR-2001; 2001US-0277340P.
PR 19-JUL-2001; 2001US-0306171P.

```
PR 13-NOV-2001; 2001US-031287P.
XX (HUMA-) HUMAN GENOME SCI INC.
PA Rosen CA, Ruben SM;
XX WPI; 2003-175238/17.
XX New human secreted proteins and nucleic acid molecules, useful for
XX preparing a diagnostic or pharmaceutical composition for diagnosing,
XX preventing or treating cancer or other hyperproliferative disorder,
XX asthma, allergies or AIDS.
XX Claim 1; SEQ ID NO 1510; 3205pp; English.
XX The invention relates to novel genes ADA39629-ADA40565 and proteins
XX ADA40566-ADA41501 for human secreted proteins, useful for preventing,
XX treating or ameliorating medical conditions e.g. by protein or gene
XX therapy. The polypeptides, nucleic acid molecules, antibodies or their
XX fragments, and agonists or antagonists that bind to the polypeptide are
XX useful for preparing a diagnostic or pharmaceutical composition for
XX diagnosing or treating cancer or other hyperproliferative disorder. The
XX polypeptides and nucleic acid molecules are also useful for detecting,
XX preventing, diagnosing, prognosticating, treating or ameliorating cancer
XX or other hyperproliferative disorders including neoplasms, autoimmune
XX disorders (e.g. diabetes, rheumatoid arthritis, systemic lupus
XX erythematosus, multiple sclerosis, autoimmune thyroiditis or haemolytic
XX anaemia), haematopoietic or haematological disorders (e.g. anaemia,
XX thrombocytopenia), allergic reactions including asthma or eczema,
XX inflammatory disorders (e.g. ischaemia-reperfusion injury, inflammatory
XX bowel disease or Crohn's disease), neurodegenerative disorders (e.g.
XX Alzheimer's disease or Parkinson's disease), cardiovascular disorders
XX (e.g. atherosclerosis, myocarditis), infectious diseases (bacterial,
XX fungal or viral infections including HIV/AIDS), or wound healing and
XX disorders of epithelial cell proliferation. The nucleic acids are also
XX useful for chromosome identification, radiation hybrid mapping or long-
XX range restriction mapping, as molecular weight markers, or as
XX hybridization or diagnostic probes. The polypeptides and antibodies are
XX useful for providing immunological probes for differential identification
XX of the tissues immunohistochemistry assays. Note: The sequence data for
XX this patent did not form part of the printed specification, but was
XX obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.
SQ Sequence 101 AA;
Query Match 7.7%; Score 71.5; DB 6; Length 101;
Best Local Similarity 27.0%; Pred. No. 4.4;
Matches 17; Conservative 10; Mismatches 19; Indels 17; Gaps 2;
QY 65 CLIIIDICIGNETELLRDFTSLGVEYQKFLHLSMHGISQILGQFA-----CMPEHR 114
DB 26 CIIIFHCVSDRSVNRRTKV-----KFVHTSVHGVGHSFVQSAPKAFKXLPVPEAVPEQK 78
QY 115 DYD 117
DB 79 DFD 81
RESULT 12
ABR47936
ID ABR47936 standard; protein; 101 AA.
XX ABR47936;
XX 12-JUN-2003 (first entry)
XX Human secreted protein, SEQ ID 827.
XX Cardiant; antiarrhythmic; antiarteriosclerotic; vasotropic; cytostatic;
XX vulnery; antiinflammatory; nootropic; neuroprotective;
XX antiparkinsonian; gene therapy; human; cardiovascular disorder.
XX
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OS Homo sapiens.
XX WO200295010-A2.
XX 28-NOV-2002.
XX 19-MAR-2002; 2002WO-US009785.
XX 21-MAR-2001; 2001US-0277340P.
XX 19-JUL-2001; 2001US-0306171P.
XX 13-NOV-2001; 2001US-0311287P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Ruben SM;
XX WPI; 2003-129429/12.
XX Novel human secreted proteins, useful for detecting, preventing,
XX diagnosing, prognosticating, treating and/or ameliorating cardiovascular
XX disorders such as arrhythmia.
XX Claim 13; SEQ ID NO 827; 1881pp; English.
XX The present invention relates to novel human secreted proteins (ABR47633-
XX ABR48145) and their coding sequences (ACC50344-ACC50856). The proteins
XX or pharmaceutical composition for diagnosing or treating a cardiovascular
XX disorder (e.g.; arrhythmia, tachycardia, cardiac arrest, coronary
XX arteriosclerosis and myocardial ischaemia), neural disorders, immune
XX system disorders, muscular disorders, reproductive disorders,
XX gastrointestinal disorders, pulmonary disorders, renal disorders,
XX proliferative disorders and/or cancerous diseases and conditions, for
XX wound healing and epithelial cell proliferation, to treat inflammation or
XX infection, for treating thrombosis and arteriosclerosis, for treating or
XX preventing neural damage which occurs in neuronal disorders or
XX neurodegenerative conditions such as Alzheimer's disease and Parkinson's
XX disease, to enhance bone and periodontal regeneration and aid in tissue
XX transplants or bone grafts, to prevent skin aging or hair loss, to
XX stimulate growth and differentiation of haematopoietic cells and bone
XX marrow cells when used in combination with other cytokines, to maintain
XX organs before transplantation or for supporting cell culture of primary
XX tissues, to increase or decrease differentiation or proliferation of
XX embryonic stem cells, or to modulate mammalian characteristics or
XX metabolism. Note: The sequence data for this patent was published in
XX electronic format and is available from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX Sequence 101 AA;
Query Match 7.7%; Score 71.5; DB 6; Length 101;
Best Local Similarity 27.0%; Pred. No. 4.4;
Matches 17; Conservative 10; Mismatches 19; Indels 17; Gaps 2;
QY 65 CLIIIDICIGNETELLRDFTSLGVEYQKFLHLSMHGISQILGQFA-----CMPEHR 114
DB 26 CIIIFHCVSDRSVNRRTKV-----KFVHTSVHGVGHSFVQSAPKAFKXLPVPEAVPEQK 78
QY 115 DYD 117
DB 79 DFD 81
RESULT 13
ABR00176
ID ABR00176 standard; protein; 101 AA.
XX ABR00176;
XX 03-APR-2003 (first entry)
XX Human gene 166 encoded secreted protein HTLEP53, SEQ ID NO:465.
XX
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Job time : 164 secs

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OM protein - protein search, using sw model

Run on: June 20, 2005, 13:44:11 ; Search time 156 Seconds
(without alignments)
435.669 Million cell updates/sec

Title: US-10-713-208-6_COPY_76_252

Perfect score: 930

Sequence: 1 KQSVQAGTSYRNVLQAAIQ.....YLAGPKMFFIQNVVSDQ 177

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1714042 seqs, 383979560 residues

Total number of hits satisfying chosen parameters: 1013902

Minimum DB seq length: 0

Maximum DB seq length: 177

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTU5_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	166	17.8	147	14	US-10-214-932-110
2	162.5	17.5	132	17	US-10-872-079-9
3	162.5	17.5	141	17	US-10-872-079-13
4	154	16.6	167	9	US-09-864-761-48728
5	130	14.0	163	9	US-09-864-761-47950
6	108	11.6	158	10	US-09-851-873-61
7	78	8.4	134	15	US-10-114-432-32
8	78	8.4	134	15	US-10-114-432-33
9	78	8.4	146	15	US-10-114-432-7
10	78	8.4	146	15	US-10-114-432-20
11	78	8.4	146	15	US-10-114-432-65

12	78	8.4	146	15	US-10-114-432-70	Sequence 70, Appl
13	78	8.4	174	15	US-10-114-432-34	Sequence 34, Appl
14	77	8.3	52	9	US-09-989-903-51	Sequence 51, Appl
15	77	8.3	52	14	US-10-068-564-51	Sequence 51, Appl
16	77	8.3	52	16	US-10-870-765-51	Sequence 51, Appl
17	76	8.2	56	9	US-09-989-903-58	Sequence 58, Appl
18	76	8.2	56	14	US-10-068-564-58	Sequence 58, Appl
19	76	8.2	56	16	US-10-870-765-58	Sequence 58, Appl
20	75.5	8.1	74	9	US-09-989-903-18	Sequence 18, Appl
21	75.5	8.1	74	14	US-10-068-564-18	Sequence 18, Appl
22	75.5	8.1	74	16	US-10-870-765-18	Sequence 18, Appl
23	75.5	8.1	77	9	US-09-989-903-25	Sequence 25, Appl
24	75.5	8.1	77	14	US-10-068-564-25	Sequence 25, Appl
25	75.5	8.1	77	16	US-10-870-765-25	Sequence 25, Appl
26	74.5	8.0	94	9	US-09-989-903-14	Sequence 14, Appl
27	74.5	8.0	94	14	US-10-068-564-14	Sequence 14, Appl
28	74.5	8.0	94	16	US-10-870-765-14	Sequence 14, Appl
29	73	7.8	39	8	US-08-459-455-45	Sequence 45, Appl
30	71.5	7.7	101	15	US-10-653-595-149	Sequence 149, App
31	71.5	7.7	102	10	US-09-397-945-149	Sequence 149, App
32	70	7.5	51	9	US-09-989-903-45	Sequence 45, Appl
33	70	7.5	51	14	US-10-068-564-45	Sequence 45, Appl
34	70	7.5	51	16	US-10-870-765-45	Sequence 45, Appl
35	68	7.3	39	9	US-09-989-903-38	Sequence 38, Appl
36	68	7.3	39	14	US-10-068-564-38	Sequence 38, Appl
37	68	7.3	39	16	US-10-870-765-38	Sequence 38, Appl
38	66.5	7.2	102	11	US-09-864-408A-1582	Sequence 1582, Ap
39	66	7.1	39	9	US-09-989-903-30	Sequence 30, Appl
40	66	7.1	39	14	US-10-068-564-30	Sequence 30, Appl
41	66	7.1	39	16	US-10-870-765-30	Sequence 30, Appl
42	66	7.1	157	15	US-10-429-872-20	Sequence 20, Appl
43	65.5	7.0	130	15	US-10-424-593-271119	Sequence 271119,
44	64.5	6.9	141	15	US-10-424-593-231330	Sequence 231330,
45	64.5	6.9	174	15	US-10-282-122A-76633	Sequence 76633, A

ALIGNMENTS

RESULT 1

US-10-214-932-110
; Sequence 110, Application US/10214932
; Publication No. US20030100707A1
; GENERAL INFORMATION:
; APPLICANT: HWANG, Inhwan
; APPLICANT: KIM, Dae Heon
; APPLICANT: LEE, Yong Jik
; TITLE OF INVENTION: SYSTEM FOR DETECTING PROTEASE
; FILE REFERENCE: APB02/US
; CURRENT APPLICATION NUMBER: US/10/214,932
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 110
; TYPE: PRT
; LENGTH: 147
; ORGANISM: Homo sapiens
US-10-214-932-110

Query Match 17.8%; Score 166; DB 14; Length 147;
Best Local Similarity 32.8%; Pred. No. 9.9e+10;
Matches 43; Conservative 22; Mismatches 49; Indels 18; Gaps 4;

QY	52	EERYKMKKPLGICLIID-----CIGNETEL--LRDTFTSLGYEVQKFLHLSM	97
DB	6	DNSYKMDYEMGLICIIINKNFKHKTGMSRSGTDVDAANLRRETRNLKYEVRKNDLTR	65
QY	98	HGISQILGQFACMPERHDVDSFVCLVSRGGSOSVGDVTHSGLPLHHTRRMFGDSCP	157
DB	66	EELVELMRDVS-KEDSHKRSFVCLLSHGEIGIFG---TNGPVDLKKITNFRGDRCR	121
QY	158	YLAGKPKMFFIQ 169	

Db 122 SLTGKPKLFIIQ 133

RESULT 2

US-10-872-079-9
; Sequence 9, Application US/10872079
; Publication No. US20050095613A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; FILE REFERENCE: 07334-280001
; CURRENT APPLICATION NUMBER: US/10/872,079
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: US/09/573,641
; PRIOR FILING DATE: 2000-05-17
; PRIOR APPLICATION NUMBER: US 60/180,021
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence
US-10-872-079-9

Query Match 17.5%; Score 162.5; DB 17; Length 132;
Best Local Similarity 40.0%; Pred. No. 2.1e-09;
Matches 42; Conservative 13; Mismatches 41; Indels 9; Gaps 2;
QY 74 ETELLRDTFTSLGYEVQKFLHLSMHGISOILGQFACMPBHRDYDSFVCLVSRGSGSQ--- 130
DB 19 DAENLRLFRSLGYEVKVKNDLTAEMVCLKRFPAKREHKDSDFVLVLLSHGSENHQ 78

QY 131 ---SVYGVGD---QTHSGLPLHHIRRMFGDSCPYLAGKPKMFFIQ 169

DB 79 FPGGIYGTGKEKVPDILSLKIFNLFGDNCPSLKGKPKLFIIQ 123

RESULT 3

US-10-872-079-13
; Sequence 13, Application US/10872079
; Publication No. US20050095613A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; FILE REFERENCE: 07334-280001
; CURRENT APPLICATION NUMBER: US/10/872,079
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: US/09/573,641
; PRIOR FILING DATE: 2000-05-17
; PRIOR APPLICATION NUMBER: US 60/180,021
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence
US-10-872-079-13

Query Match 17.5%; Score 162.5; DB 17; Length 141;
Best Local Similarity 40.0%; Pred. No. 2.3e-09;
Matches 42; Conservative 13; Mismatches 41; Indels 9; Gaps 2;
QY 74 ETELLRDTFTSLGYEVQKFLHLSMHGISOILGQFACMPBHRDYDSFVCLVSRGSGSQ--- 130
DB 28 DAENLRLFRSLGYEVKVKNDLTAEMVCLKRFPAKREHKDSDFVLVLLSHGSENHQ 87

QY 131 ---SVYGVGD---QTHSGLPLHHIRRMFGDSCPYLAGKPKMFFIQ 169
DB 88 FPGGIYGTGKEKVPDILSLKIFNLFGDNCPSLKGKPKLFIIQ 132

RESULT 4

US-09-864-761-48728
; Sequence 48728, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aemica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 48728
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC007256.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2
; OTHER INFORMATION: EST HUMAN HIT: BE271526.1, EVALUATE 2.00e-98
; OTHER INFORMATION: SWISSPROT HIT: Q14790, EVALUATE 2.00e-99
US-09-864-761-48728

Query Match 16.6%; Score 154; DB 9; Length 167;
Best Local Similarity 35.4%; Pred. No. 2.4e-08;
Matches 35; Conservative 18; Mismatches 38; Indels 8; Gaps 3;

QY 78 LRDFTSLGVEYQKFLHLSMHGISOILQGFACMPEDRDYDFVCLVSRGSGSQSVYGVDDQ 137
DB 2 LTTTEELHFEIKPHDDCTVEQIYELIKYQLM-DHSNMDCFICILSHGDKGIYGTGD 60
QY 138 THSGPLHHRMFMGSDCPYLAKPKMFFIQ-----NY 171
DB 61 QEA--PIVELTSQFTGLKCPSLAGPKVPFFIQACQGDNY 97

RESULT 5

US-09-864-761-47950
; Sequence 47950, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aomicca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1

SEQ ID NO 47950
LENGTH: 163
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC007283.3
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.1
OTHER INFORMATION: EST HUMAN HIT: BE271526.1, EVALUE 4.00e-31
OTHER INFORMATION: SWISSPROT HIT: Q92851, EVALUE 3.00e-94
US-09-864-761-47950

Query Match 14.0%; Score 130; DB 9; Length 163;
Best Local Similarity 33.3%; Pred. No. 9.7e-06;
Matches 31; Conservative 17; Mismatches 43; Indels 2; Gaps 1;
QY 77 LRDFTSLGVEYQKFLHLSMHGISOILQGFACMPEDRDYDFVCLVSRGSGSQSVYGVDD 136
DB 1 ILSHVFWGLGFTVHTNNVTKVEMEMVLQKQCNPAHADGDCFVFCILTHGRFGAVYSSD 60
QY 137 QTHSGPLHHRMFMGSDCPYLAKPKMFFIQ 169
DB 61 E--ALIPIREINSHFTALQCPRLAEKPKLFFTIQ 91

RESULT 6

US-09-851-873-61
; Sequence 61, Application US/09851873
; Publication No. US20030165488A1
; GENERAL INFORMATION:
; APPLICANT: Kletzien, Rolf F
; APPLICANT: Reardon, Ilene M
; APPLICANT: Welland, Katherine L
; TITLE OF INVENTION: HUMAN CASPASE-12 MATERIALS AND METHODS
; FILE REFERENCE: 28341/00233
; CURRENT APPLICATION NUMBER: US/09/851,873
; CURRENT FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 61
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-851-873-61

Query Match 11.6%; Score 108; DB 10; Length 158;
Best Local Similarity 26.4%; Pred. No. 0.0023;
Matches 42; Conservative 19; Mismatches 70; Indels 28; Gaps 4;
QY 26 PSNFRFPVKKSIOSEAFLPQSIPEERYKMKSPGLGCLIDC-----IGNE 74
DB 11 PHAHFHELTGRA-----DEIYPMEKERTCLALNTRNKEFNYLHNRNGSE 57
QY 75 TELL--RDTFTSLGVEYQKFLHLSMHGISOILQGFACMPEDRDYDFVCLVSRGSGSQSVY 133
DB 58 LLLGMDLLENLGVSVIKESLTAQEMETALQFPAHPEHQSSDSTFLVFMHSHILNGIC 117
QY 134 GV---DQTHSGPLHHRMFMGSDCPYLAKPKMFFIQ 169
DB 118 GTKHWDQPDVLDHDTIFEINNRNCQSLKDKPKVIMQ 156

RESULT 7

US-10-114-432-32
; Sequence 32, Application US/10114432
; Publication No. US20040019915A1
; GENERAL INFORMATION:
; APPLICANT: Challita-Sid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Robert K.
; APPLICANT: Ge, Wangmao
; APPLICANT: Jakobivits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; TITLE OF INVENTION: ENTITLED 213P111 USEFUL IN TREATMENT AND
; TITLE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20066.00
; CURRENT APPLICATION NUMBER: US/10/114,432
; CURRENT FILING DATE: 2002-04-01
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 134
; TYPE: PRT

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; ORGANISM: Homo Sapiens
US-10-114-432-32

Query Match      8.4%; Score 78; DB 15; Length 134;
Best Local Similarity 25.6%; Pred. No. 3.5;
Matches 34; Conservative 22; Mismatches 61; Indels 16; Gaps 6;

Qy 47 POSIPEERYKMKSKPLGICLIIDCI-----GNETEL--LRDTFTSLGYEVQKFLHLSMHG 99
Db 4 PRSLEEEKYDMSGARLAIL---CVTKAREGSEEDLDALEHMFRLQRFESTMKRDPPTAEQ 60

Qy 100 ISQILGQFACMPHEHRDYSFVC---VLVSRGSGSVYGVQDTHSGLPLHHRMFMGDSG 156
Db 61 FQEELEKFOQAIDSRE-DPVSCAFVWLMAHGREGLKGED--GEMVKLENLFEALNNKNC 117

Qy 157 PYLAGKPKMFFIQ 169
Db 118 QALRAKPKVYIIQ 130

RESULT 8
US-10-114-432-33
; Sequence 33, Application US/10114432
; Publication No. US20040019915A1
; GENERAL INFORMATION:
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Robert K.
; APPLICANT: Ge, Wangmao
; APPLICANT: Jakobivits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; TITLE OF INVENTION: ENTITLED 213PIF11 USEFUL IN TREATMENT AND
; TITLE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20066.00
; CURRENT APPLICATION NUMBER: US/10/114,432
; CURRENT FILING DATE: 2002-04-01
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-114-432-33

Query Match      8.4%; Score 78; DB 15; Length 134;
Best Local Similarity 25.6%; Pred. No. 3.5;
Matches 34; Conservative 22; Mismatches 61; Indels 16; Gaps 6;

Qy 47 POSIPEERYKMKSKPLGICLIIDCI-----GNETEL--LRDTFTSLGYEVQKFLHLSMHG 99
Db 4 PRSLEEEKYDMSGARLAIL---CVTKAREGSEEDLDALEHMFRLQRFESTMKRDPPTAEQ 60

Qy 100 ISQILGQFACMPHEHRDYSFVC---VLVSRGSGSVYGVQDTHSGLPLHHRMFMGDSG 156
Db 61 FQEELEKFOQAIDSRE-DPVSCAFVWLMAHGREGLKGED--GEMVKLENLFEALNNKNC 117

Qy 157 PYLAGKPKMFFIQ 169
Db 118 QALRAKPKVYIIQ 130

RESULT 9
US-10-114-432-7
; Sequence 7, Application US/10114432
; Publication No. US20040019915A1
; GENERAL INFORMATION:
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Robert K.
```

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; APPLICANT: Ge, Wangmao
; APPLICANT: Jakobivits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; TITLE OF INVENTION: ENTITLED 213PIF11 USEFUL IN TREATMENT AND
; TITLE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20066.00
; CURRENT APPLICATION NUMBER: US/10/114,432
; CURRENT FILING DATE: 2002-04-01
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-114-432-7

Query Match      8.4%; Score 78; DB 15; Length 146;
Best Local Similarity 25.6%; Pred. No. 4;
Matches 34; Conservative 22; Mismatches 61; Indels 16; Gaps 6;

Qy 47 POSIPEERYKMKSKPLGICLIIDCI-----GNETEL--LRDTFTSLGYEVQKFLHLSMHG 99
Db 4 PRSLEEEKYDMSGARLAIL---CVTKAREGSEEDLDALEHMFRLQRFESTMKRDPPTAEQ 60

Qy 100 ISQILGQFACMPHEHRDYSFVC---VLVSRGSGSVYGVQDTHSGLPLHHRMFMGDSG 156
Db 61 FQEELEKFOQAIDSRE-DPVSCAFVWLMAHGREGLKGED--GEMVKLENLFEALNNKNC 117

Qy 157 PYLAGKPKMFFIQ 169
Db 118 QALRAKPKVYIIQ 130

RESULT 10
US-10-114-432-20
; Sequence 20, Application US/10114432
; Publication No. US20040019915A1
; GENERAL INFORMATION:
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Robert K.
; APPLICANT: Ge, Wangmao
; APPLICANT: Jakobivits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; TITLE OF INVENTION: ENTITLED 213PIF11 USEFUL IN TREATMENT AND
; TITLE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20066.00
; CURRENT APPLICATION NUMBER: US/10/114,432
; CURRENT FILING DATE: 2002-04-01
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-114-432-20

Query Match      8.4%; Score 78; DB 15; Length 146;
Best Local Similarity 25.6%; Pred. No. 4;
Matches 34; Conservative 22; Mismatches 61; Indels 16; Gaps 6;

Qy 47 POSIPEERYKMKSKPLGICLIIDCI-----GNETEL--LRDTFTSLGYEVQKFLHLSMHG 99
Db 4 PRSLEEEKYDMSGARLAIL---CVTKAREGSEEDLDALEHMFRLQRFESTMKRDPPTAEQ 60

Qy 100 ISQILGQFACMPHEHRDYSFVC---VLVSRGSGSVYGVQDTHSGLPLHHRMFMGDSG 156
Db 61 FQEELEKFOQAIDSRE-DPVSCAFVWLMAHGREGLKGED--GEMVKLENLFEALNNKNC 117

Qy 157 PYLAGKPKMFFIQ 169
Db 118 QALRAKPKVYIIQ 130
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; SEQ ID NO 51
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-989-903-51

Query Match      8.3%; Score 77; DB 9; Length 52;
Best Local Similarity 50.0%; Pred. No. 1.3;
Matches 13; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 144 LHHRRMFMGDSCPYLAGKPKMFFIQ 169
   ::: ||| |||:|||||
Db 4 IYDLTSYFTGSKCPSLSGKPKIFFIQ 29

RESULT 15
US-10-068-564-51
; Sequence 51, Application US/10068564
; Publication No. US20030040096A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING
; TITLE OF INVENTION: AND METHODS OF USE
; FILE REFERENCE: 480140.434C2
; CURRENT APPLICATION NUMBER: US/10/068,564
; CURRENT FILING DATE: 2002-02-05
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-068-564-51

Query Match      8.3%; Score 77; DB 14; Length 52;
Best Local Similarity 50.0%; Pred. No. 1.3;
Matches 13; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 144 LHHRRMFMGDSCPYLAGKPKMFFIQ 169
   ::: ||| |||:|||||
Db 4 IYDLTSYFTGSKCPSLSGKPKIFFIQ 29

Search completed: June 20, 2005, 13:57:30
Job time : 157 secs
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Result No.	Score	Query			DB	ID	Description
		Match	Length				
1	166	17.8	148	3	US-08-964-308-11	Sequence 11, Appl	
2	166	17.8	148	3	US-08-964-313-11	Sequence 11, Appl	
3	166	17.8	148	3	US-09-069-138-11	Sequence 11, Appl	
4	108	11.6	158	4	US-09-851-873-61	Sequence 61, Appl	
5	77	8.3	52	3	US-09-187-789-51	Sequence 51, Appl	
6	77	8.3	52	4	US-09-139-600-46	Sequence 46, Appl	
7	77	8.3	52	4	US-09-989-903-51	Sequence 51, Appl	
8	76	8.2	56	3	US-09-187-789-58	Sequence 58, Appl	
9	76	8.2	56	4	US-09-139-600-53	Sequence 53, Appl	
10	76	8.2	56	4	US-09-989-903-58	Sequence 58, Appl	
11	75.5	8.1	74	3	US-09-187-789-18	Sequence 18, Appl	
12	75.5	8.1	74	4	US-09-139-600-13	Sequence 13, Appl	
13	75.5	8.1	74	4	US-09-989-903-18	Sequence 18, Appl	
14	75.5	8.1	77	3	US-09-187-789-25	Sequence 25, Appl	
15	75.5	8.1	77	3	US-09-139-600-20	Sequence 20, Appl	
16	75.5	8.1	77	4	US-09-989-903-25	Sequence 25, Appl	
17	75	8.1	147	4	US-09-270-767-33680	Sequence 33680, A	
18	75	8.1	147	4	US-09-270-767-48897	Sequence 48897, A	
19	74.5	8.0	94	3	US-09-187-789-14	Sequence 14, Appl	
20	74.5	8.0	94	4	US-09-139-600-9	Sequence 9, Appl	
21	74.5	8.0	94	4	US-09-989-903-14	Sequence 14, Appl	
22	73	7.8	39	3	US-08-258-287B-46	Sequence 46, Appl	
23	73	7.8	39	3	US-08-368-704C-45	Sequence 45, Appl	
24	70.5	7.6	173	4	US-09-540-236-3337	Sequence 3337, Ap	
25	70	7.5	51	3	US-09-187-789-45	Sequence 45, Appl	
26	70	7.5	51	4	US-09-139-600-40	Sequence 40, Appl	
27	70	7.5	51	4	US-09-989-903-45	Sequence 45, Appl	

Db 7 DNSYKMDYPEMGLCIIINNKNFHKSTGMTSRSGTDVDAANLRETFNRLKYEVNRKNLDR 66
QY 98 HGISQILGQACMPHEHRDYSFVCLVSRGGSQSVYGVDTHTSGLPLHHIRRMFMGDCSCP 157
Db 67 EEIVELMRDVS-KEDHSKRSSFVCLLSHGEGIIIFG---TNGPVDLKKITNFFRGDRCR 122
QY 158 YLAGPKPMFFIQ 169
Db 123 SLTGPKPLFIQ 134

RESULT 2
US-08-964-313-11
; Sequence 11, Application US/08964313
; Patent No. 6114132
; GENERAL INFORMATION:
; APPLICANT: DESMARAIS, SYLVIE
; APPLICANT: FRIESEN, RICHARD
; APPLICANT: GRESSER, MICHAEL
; APPLICANT: KENNEDY, BRIAN
; APPLICANT: NICHOLSON, DONALD
; APPLICANT: RAMACHANDRAN, CHIDAMBARAN
; APPLICANT: SKOREY, KATHRYN
; APPLICANT: FORD-HUTCHINSON, ANTHONY
; TITLE OF INVENTION: PHOSPHATASE BINDING ASSAY
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PHILIPPE L. DURETTE - MERCK & CO., INC.
; STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
; CITY: RAHWAY
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/964,313
; FILING DATE: 04-NOV-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/030,408
; FILING DATE: 04-NOV-1996
; APPLICATION NUMBER: PCT/CA97/00825
; FILING DATE: 03-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: DURETTE, PHILIPPE L.
; REGISTRATION NUMBER: 35,125
; REFERENCE/DOCKET NUMBER: 19824Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-4568
; TELEFAX: 732-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 148 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-964-313-11

Query Match 17.8%; Score 166; DB 3; Length 148;
Best Local Similarity 32.6%; Pred. No. 2.1e-12;
Matches 43; Conservative 22; Mismatches 49; Indels 18; Gaps 4;

QY 52 EERYKMKSKPLGICLIID-----CIGNETEL--LRDTFTSLGVEYQKFLHLSM 97
Db 7 DNSYKMDYPEMGLCIIINNKNFHKSTGMTSRSGTDVDAANLRETFNRLKYEVNRKNLDR 66

QY 98 HGISQILGQACMPHEHRDYSFVCLVSRGGSQSVYGVDTHTSGLPLHHIRRMFMGDCSCP 157
Db 67 EEIVELMRDVS-KEDHSKRSSFVCLLSHGEGIIIFG---TNGPVDLKKITNFFRGDRCR 122
QY 158 YLAGPKPMFFIQ 169
Db 123 SLTGPKPLFIQ 134

Db 67 EEIVELMRDVS-KEDHSKRSSFVCLLSHGEGIIIFG---TNGPVDLKKITNFFRGDRCR 122
QY 158 YLAGPKPMFFIQ 169
Db 123 SLTGPKPLFIQ 134

RESULT 3
US-09-069-138-11
; Sequence 11, Application US/09069138
; Patent No. 6348572
; GENERAL INFORMATION:
; APPLICANT: DESMARAIS, SYLVIE
; APPLICANT: DUFRESNE, CLAUDE
; APPLICANT: FRIESEN, RICHARD
; APPLICANT: LEBLANC, YVES
; APPLICANT: ROY, PATRICK
; APPLICANT: YOUNG, ROBERT N.
; APPLICANT: ZAMBONI, ROBERT
; TITLE OF INVENTION: NEW LIGANDS FOR PHOSPHATASE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PHILIPPE L. DURETTE - MERCK & CO., INC.
; STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
; CITY: RAHWAY
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Diskette
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/069,138
; FILING DATE: 29-APR-1998
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: DURETTE, PHILIPPE L.
; REGISTRATION NUMBER: 35,125
; REFERENCE/DOCKET NUMBER: 19840YIA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-4568
; TELEFAX: 732-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 148 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-069-138-11

Query Match 17.8%; Score 166; DB 3; Length 148;
Best Local Similarity 32.6%; Pred. No. 2.1e-12;
Matches 43; Conservative 22; Mismatches 49; Indels 18; Gaps 4;

QY 52 EERYKMKSKPLGICLIID-----CIGNETEL--LRDTFTSLGVEYQKFLHLSM 97
Db 7 DNSYKMDYPEMGLCIIINNKNFHKSTGMTSRSGTDVDAANLRETFNRLKYEVNRKNLDR 66

QY 98 HGISQILGQACMPHEHRDYSFVCLVSRGGSQSVYGVDTHTSGLPLHHIRRMFMGDCSCP 157
Db 67 EEIVELMRDVS-KEDHSKRSSFVCLLSHGEGIIIFG---TNGPVDLKKITNFFRGDRCR 122
QY 158 YLAGPKPMFFIQ 169
Db 123 SLTGPKPLFIQ 134

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; TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING
; TITLE OF INVENTION: AND METHOD OF USE
; FILE REFERENCE: 480140.434
; CURRENT APPLICATION NUMBER: US/09/139,600
; CURRENT FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-139-600-46

Query Match      8.3%; Score 77; DB 4; Length 52;
Best Local Similarity 50.0%; Pred. No. 0.052;
Matches 13; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Qy 144 LHHIRMFMGDSCPYLAGKPKMFFIQ 169
Db 4 IYDLTSYFTGSKCPSLSGKPKIFFIQ 29

RESULT 7
US-09-989-903-51
; Sequence 51, Application US/09989903
; Patent No. 6797812
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING
; TITLE OF INVENTION: AND METHODS OF USE
; FILE REFERENCE: 480140.434C1
; CURRENT APPLICATION NUMBER: US/09/989,903
; CURRENT FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-989-903-51

Query Match      8.3%; Score 77; DB 4; Length 52;
Best Local Similarity 50.0%; Pred. No. 0.052;
Matches 13; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Qy 144 LHHIRMFMGDSCPYLAGKPKMFFIQ 169
Db 4 IYDLTSYFTGSKCPSLSGKPKIFFIQ 29

RESULT 8
US-09-187-789-58
; Sequence 58, Application US/09187789
; Patent No. 6340740
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING
; TITLE OF INVENTION: AND METHODS OF USE
; FILE REFERENCE: 480140.434C1
; CURRENT APPLICATION NUMBER: US/09/187,789
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 58
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-187-789-58

Query Match      8.2%; Score 76; DB 3; Length 56;
Best Local Similarity 53.6%; Pred. No. 0.077;
Matches 13; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Qy 144 LHHIRMFMGDSCPYLAGKPKMFFIQ 169
Db 4 IYDLTSYFTGSKCPSLSGKPKIFFIQ 29

RESULT 6
US-09-139-600-46
; Sequence 46, Application US/09139600
; Patent No. 6432628
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING
; TITLE OF INVENTION: AND METHOD OF USE
; FILE REFERENCE: 480140.434
; CURRENT APPLICATION NUMBER: US/09/139,600
; CURRENT FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-139-600-46

Query Match      8.3%; Score 77; DB 4; Length 52;
Best Local Similarity 50.0%; Pred. No. 0.052;
Matches 13; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Qy 144 LHHIRMFMGDSCPYLAGKPKMFFIQ 169
Db 4 IYDLTSYFTGSKCPSLSGKPKIFFIQ 29

RESULT 4
US-09-851-873-61
; Sequence 61, Application US/09851873
; Patent No. 6833248
; GENERAL INFORMATION:
; APPLICANT: Kletzien, Rolf F
; APPLICANT: Reardon, Ilene M
; APPLICANT: Weiland, Katherine L
; TITLE OF INVENTION: HUMAN CASPASE-12 MATERIALS AND METHODS
; FILE REFERENCE: 28341/00233
; CURRENT APPLICATION NUMBER: US/09/851,873
; CURRENT FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 61
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-851-873-61

Query Match      11.6%; Score 108; DB 4; Length 158;
Best Local Similarity 26.4%; Pred. No. 3.9e-05;
Matches 42; Conservative 19; Mismatches 70; Indels 28; Gaps 4;

Qy 26 PSNNFPEPVKSIQSEAFQSPPEERYKMKSPGLGCLIIDC-----IGNE 74
Db 11 PHAFHELKTKRA-----DEIYPVMEKERTCTALNIRNKEFNLYLHNRNGSE 57

Qy 75 TELL-RDTFTSLGVEYQKFLHLSMHGISOILGQFACMPEDHRDYDFVCVLVSRGSSQSVY 133
Db 58 LDLGLMDLLENLGYSVVIKESITQAQEMETALQFAAHPHQSSDSTFLVFMHSHLILNGIC 117

Qy 134 GV---DQTHSGSLPHHRRMFMGDSCPYLAGKPKMFFIQ 169
Db 118 GTRKHQDEPDLVHDDTIFEIFENNRNCQSLKDKPKVILMQ 156

RESULT 5
US-09-187-789-51
; Sequence 51, Application US/09187789
; Patent No. 6340740
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING
; TITLE OF INVENTION: AND METHODS OF USE
; FILE REFERENCE: 480140.434C1
; CURRENT APPLICATION NUMBER: US/09/187,789
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-187-789-51

Query Match      8.3%; Score 77; DB 3; Length 52;
Best Local Similarity 50.0%; Pred. No. 0.052;
Matches 13; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Qy 144 LHHIRMFMGDSCPYLAGKPKMFFIQ 169
Db 4 IYDLTSYFTGSKCPSLSGKPKIFFIQ 29

RESULT 3
US-09-187-789-51
; Sequence 51, Application US/09187789
; Patent No. 6340740
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING
; TITLE OF INVENTION: AND METHODS OF USE
; FILE REFERENCE: 480140.434C1
; CURRENT APPLICATION NUMBER: US/09/187,789
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-187-789-51

Query Match      8.3%; Score 77; DB 3; Length 52;
Best Local Similarity 50.0%; Pred. No. 0.052;
Matches 13; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Qy 144 LHHIRMFMGDSCPYLAGKPKMFFIQ 169
Db 4 IYDLTSYFTGSKCPSLSGKPKIFFIQ 29

RESULT 2
US-09-187-789-51
; Sequence 51, Application US/09187789
; Patent No. 6340740
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING
; TITLE OF INVENTION: AND METHODS OF USE
; FILE REFERENCE: 480140.434C1
; CURRENT APPLICATION NUMBER: US/09/187,789
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-187-789-51

Query Match      8.3%; Score 77; DB 3; Length 52;
Best Local Similarity 50.0%; Pred. No. 0.052;
Matches 13; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Qy 144 LHHIRMFMGDSCPYLAGKPKMFFIQ 169
Db 4 IYDLTSYFTGSKCPSLSGKPKIFFIQ 29

RESULT 1
US-09-187-789-51
; Sequence 51, Application US/09187789
; Patent No. 6340740
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING
; TITLE OF INVENTION: AND METHODS OF USE
; FILE REFERENCE: 480140.434C1
; CURRENT APPLICATION NUMBER: US/09/187,789
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-187-789-51

Query Match      8.3%; Score 77; DB 3; Length 52;
Best Local Similarity 50.0%; Pred. No. 0.052;
Matches 13; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Qy 144 LHHIRMFMGDSCPYLAGKPKMFFIQ 169
Db 4 IYDLTSYFTGSKCPSLSGKPKIFFIQ 29

```



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; LENGTH: 74
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-989-903-18

Query Match
Best Local Similarity 30.6%; DB 4; Length 74;
Matches 19; Conservative 11; Mismatches 29; Indels 3; Gaps 1;

QY      111 PEHRDVDSFVCVLVRGSGSVGVGDTHSGLPLHH---TRRPMFGSDCPYLACKPKQPF 167
      ||||: ||||: ||||: ||||: ||||: ||||: ||||: ||||: ||||:
Db      1 PEHQSSDSTELVFMMSGHILEGICGVKRNKKPDVLHDDTTFIKTFNNNSCRSLRNKPILI 60

QY      168 IQ 169
      :
Db      61 MO 62

```

Db 1 PEHQSSDSTFLVFM SHGILEGICGVKHRNKKPDVLHDDTIFKIFNNSNCRSLRNKPKILI 60

```

Query Match      8.1%; Score 75.5; DB 3; Length 77;
Best Local Similarity 34.4%; Pred.No 0.14;
Matches 22; Conservative 8; Mismatches 27; Indels 7; Gaps 2;

QY    111 PEHRDVDSFCVILVRGGSQSVGVDOTHSG-----LPLHHRRMFMGSDCPYLAKPKKM 165
      ||||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db     1  PEKHTSDSTELFWMSHGIGEGICGT--TYSNEVSIDLKVDITFQMNTWLKCPSLKDKPKV  58

QY    166 FFIQ 169
      ||
Db     59 IIIO 62
```

	Query Match	8.1%;	Score 75.5;	DB 3;	Length 77;	
	Best Local Similarity	34.4%;	Pred. No. 0.14;			
	Matches 22;	Conservative 8;	Mismatches 27;	Indels 7;	Gaps 2;	
QY	111	PEHRDVDSFCVILVRGGSQSVGVDOETHSG-----LPLHHRRMFMGSDSCPYLAKPKKM	165			
		: : : : : : : : : :				
Dd	1	PEKHTSDSTELFWMSHGIGEGICGT--TYSNEVSIDLKVDITFQMNTWLKCPSLKDKPKV	58			
QY	166	FFIQ	169			
Dd	59	IIO	62			

Query Match	8.1%;	Score 75.5;	DB 4;	Length 77;
Best Local Similarity	34.4%;	Pred. No. 0.14;		

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Result No.	Score	Query %		DB	ID	Description
		Match	Length			
1	50	10.1	34	2	S44828	F54F2.3 protein -
2	49	9.9	74	2	AG2533	hypothetical prote
3	48.5	9.8	68	2	AD2173	hypothetical prote
4	48.5	9.8	96	2	G33730	Ig kappa chain V r
5	48	9.7	51	2	H82689	hypothetical prote
6	47.5	9.6	65	1	XTPC1	acrosin inhibitor
7	47.5	9.6	71	2	S20194	sperm-associated a
8	47.5	9.6	85	2	F86389	probable DNA-bind
9	47.5	9.6	92	2	A26395	T-cell receptor be
10	46	9.3	42	2	T07285	hypothetical prote
11	46	9.3	69	2	PH1080	Ig light chain V r
12	46	9.3	80	2	T01450	limonene cyclase h
13	45	9.3	87	2	A64429	hypothetical prote
14	45.5	9.2	69	2	E25647	hypothetical lc pr
15	44.5	9.0	58	2	AC1869	hypothetical prote
16	44.5	9.0	72	2	E43259	H+-transporting tw
17	44.5	9.0	88	2	S66287	saeacin B precursor
18	44.5	9.0	92	2	AB2021	hypothetical prote
19	44	8.9	68	2	C97874	degenerate transpo
20	44	8.9	72	2	T31010	hypothetical prote
21	43.5	8.8	60	2	S68769	short neurotoxin -
22	43.5	8.8	82	2	T04476	acclimation protei
23	43.5	8.8	84	2	T17637	hypothetical prote
24	43	8.7	66	2	H82783	hypothetical prote
25	43	8.7	67	2	B35063	hypothetical prote
26	43	8.7	71	2	T29378	LuN-32 protein - C
27	43	8.7	92	2	AF1919	hypothetical prote
28	43	8.7	96	2	T45337	hypothetical prote
29	42.5	8.6	58	2	B43928	probable collagen

Best Local Simi

Query Match 9.9%; Score 49; DB 2; Length 74;
Best Local Similarity 47.6%; Pred. No. 1.2e+02;
Matches 10; Conservative 2; Mismatches 7; Indels

A;Accession: S20394
A;Molecule type: protein
A;Residues: 1-71 <JON>
A;Experimental source: spermatozoa
A;Accession: S20395
A;Molecule type: protein
A;Residues: 3-68 <J02>
A;Experimental source: spermatozoa
A;Note: these proteins were not glycosylated
R;Calvete, J.J.; Dostalova, Z.; Sanz, L.; Adermann, K.; Thole, H.H.; Toepfer-Petersen, H.
FEBS Lett. 379, 207-211, 1996
A;Title: Mapping the heparin-binding domain of boar spermadhesins.
A;Reference number: S68648; MUID:96184566; PMID:8603690
A;Accession: S68652
A;Molecule type: protein
A;Residues: 1-11, 'X', 13, 18-21, 'X', 23-26 <CAL>
C;Superfamily: pancreatic secretory trypsin inhibitor; Kazal proteinase inhibitor homolog
C;Keywords: semen; serine proteinase inhibitor; sperm; testis
F;1-71/Product: sperm-associated acrosin inhibitor, minor form #status experimental <WAT>
F;1-68, 70-71/Product: sperm-associated acrosin inhibitor, long form #status experimental
F;3-68, 70-71/Product: sperm-associated acrosin inhibitor, short form #status experimental
F;10-62/Domain: Kazal proteinase inhibitor homolog <KPI>
F;12-44, 22-41, 30-62/Disulfide bonds: #status experimental
F;50/Inhibitory site: Arg (acrosin, trypsin) #status predicted

Query Match 9.6%; Score 47.5; DB 2; Length 71;
Best Local Similarity 30.9%; Pred. No. 1.7e+02;
Matches 17; Conservative 12; Mismatches 15; Indels 11; Gaps 4;

QY 20 KAOKRGGLCTVHREADFWSLCTADMSLL----EQSHSPSLYLQCLSKL-ROER 69
Db 5 KTRKEPDCVYRSHLFF---CTREMPICGTNGKSYANPCIF--CSEKLGKNEK 53

RESULT 8
F86389
probable DNA-binding protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: F86389
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.E.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: F86389
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-85 <STO>
A;Cross-references: UNIPROT:Q9C676; GB:AE005172; NID:gl1079506; PIDN:AG29217.1; GSPDB:G
C;Genetics:
A;Map position: 1
C;Superfamily: transcription factor squa; serum response factor DNA-binding domain homol

Query Match 9.6%; Score 47.5; DB 2; Length 85;
Best Local Similarity 28.3%; Pred. No. 2.1e+02;
Matches 13; Conservative 10; Mismatches 20; Indels 3; Gaps 1;

QY 6 LLEVDGPMKNVFFKAKRGKGLCTVHREADFWSLCTADMSLLRQSH 51
Db 8 LKRIENKINQVTFKRRTGLL---KKAQEIISVLCDAEIVLVPFSH 50

RESULT 9
A26395
T-cell receptor beta chain V-D-J-C0 regions (NZW8) - mouse (fragment)
C;Species: Mus musculus (house mouse)

C;Date: 02-Jun-1988 #sequence_revision 02-Jun-1988 #text_change 30-May-1997
C;Accession: A26395
R;Behlke, M.A.; Loh, D.Y.
Nature 322, 379-382, 1986
A;Title: Alternative splicing of murine T-cell receptor beta-chain transcripts.
A;Reference number: A26395; MUID:86284983; PMID:3488509
A;Accession: A26395
A;Molecule type: mRNA
A;Residues: 1-92 <BEH>
A;Cross-references: GB:M30880
A;Note: alternative splicing gives rise to transcripts containing an additional exon betw
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: T-cell receptor

Query Match 9.6%; Score 47.5; DB 2; Length 92;
Best Local Similarity 30.0%; Pred. No. 2.3e+02;
Matches 27; Conservative 6; Mismatches 26; Indels 31; Gaps 6;

QY 5 SLLEVDGPMKNVFFKAKRGK-----LCTVHREADFFWS---LCT 41
Db 7 SLME-DGGAPKD-RFAEMLNSSFTLKIQTPEKDSAVYLCASTRATEVFFGKGRLLTV 64

QY 42 ADMSLLEQSHSPSLYLQCLSKLROERGT 71
Db 65 VGLRLSYASHHS-SLTSQC-----RSECGT 88

RESULT 10
T07285
hypothetical protein 42b - Chlorella vulgaris chloroplast
C;Species: chloroplast Chlorella vulgaris
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000
C;Accession: T07285
R;Wakasugi, T.; Nagai, T.; Kapoor, M.; Sugita, M.; Ito, S.; Tsudzuki, J.; Nakas
Proc. Natl. Acad. Sci. U.S.A. 94, 5967-5972, 1997
A;Title: Complete nucleotide sequence of the chloroplast genome from the green alga Chlo
A;Reference number: Z15985; MUID:97303241; PMID:9159184
A;Accession: T07285
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-42 <WAK>
A;Cross-references: EMBL:AB001684; NID:g2224352; PIDN:BAAS7933.1; PID:g2224449
C;Genetics:
A;Genome: chloroplast
C;Keywords: chloroplast

Query Match 9.3%; Score 46; DB 2; Length 42;
Best Local Similarity 28.2%; Pred. No. 1.4e+02;
Matches 11; Conservative 9; Mismatches 9; Indels 10; Gaps 1;

QY 48 EQSHSPSLYLQCLSKLROERGTIPGSGITKSMHFS 86
Db 8 KKSQYTCQSYLTVTDQELSEE-----EEDWFFS 36

RESULT 11
PHI080
Ig light chain V region (clone 165.60) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 15-Jun-1996
C;Accession: PHI080
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cr
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PHI080
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-69 <TIL>
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin

```
Query Match          9.3%; Score 46; DB 2; Length 69;
Best Local Similarity 28.0%; Pred. No. 2.5e+02;
Matches 14; Conservative 6; Mismatches 18; Indels 12; Gaps 1;

QY 48 EQSHSPSLYLQCLSQKLRQERTIPGSGI-----TESKDMHF 85
Db 9 QKSHESPLLIKYASOSIGSPRFGSGGDTFLSINSVETEDFGMYF 58

RESULT 12
T01450
limonene cyclase homolog F2401.12 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 15-Mar-2004
C:Accession: T01450
R:Shinn, P.; Buehler, E.; Dewar, K.; Feng, J.; Kim, C.; Li, Y.; Sun, H.; Conway, A.; Con-
eologis, A.; Ecker, J.R.
submitted to the EMBL Data Library, January 1998
A:Description: Genomic sequence for Arabidopsis thaliana BAC F2401.
A:Reference number: Z14211
A:Accession: T01450
A>Status: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-80 <SHI>
A:Cross-references: EMBL:AC003113; NID:g2689438; PID:g2781356; GSPDB:GN00059; ATSP:F2401
A:Experimental source: cultivar Columbia
C:Genetic:
A:Gene: ATSP:F2401.12
A:Map position: 1
C:Superfamily: vetispiradiene synthase 1

Query Match          9.3%; Score 46; DB 2; Length 80;
Best Local Similarity 26.5%; Pred. No. 3e+02;
Matches 9; Conservative 9; Mismatches 16; Indels 16; Gaps 0;

QY 49 QSHSPSLYLQCLSQKLRQERTIPGSGITESKD 82
Db 37 KSPSLPERLIKMDIKNVRNLSTMGCGVLKYND 70

RESULT 13
A64429
hypothetical protein MJ1034 - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: A64429
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C
A>Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A:Reference number: A64300; MUID:96337999; PMID:8688087
A:Accession: A64429
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-87 <BUL>
A:Cross-references: UNIPROT:Q58440; GB:U67546; GB:L77117; NID:g1591687; PIDN:ARB999038.1;
C:Genetic:
A:Map position: FOR966052-966315
C:Superfamily: conserved hypothetical protein MJ1034

Query Match          9.3%; Score 46; DB 2; Length 87;
Best Local Similarity 26.3%; Pred. No. 3.3e+02;
Matches 10; Conservative 12; Mismatches 12; Indels 4; Gaps 2;

QY 7 LEVDGPAMKNVEFKAQKRG-LCTVHREADF---FWSLC 40
Db 24 LAIEKPSLKDIEKALKKLGLEPKIYRKRYPRQHWIEIC 61

RESULT 14
E25647
```

```
hypothetical lc protein - phage PA2
C:Species: phage PA2
A>Note: host Escherichia coli
C>Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 09-Jul-2004
C:Accession: E25647
R:Blasband, A.J.; Marcotte Jr., W.R.; Schnaitman, C.A.
J. Biol. Chem. 261, 12723-12732, 1986
A>Title: Structure of the lc and nmPC outer membrane porin protein genes of lambdaoid bact
A:Reference number: A25647; MUID:86304457; PMID:3017988
A:Accession: E25647
A:Molecule type: DNA
A:Residues: 1-69 <BLA>
A:Cross-references: UNIPROT:Q38586; GB:J02580; NID:g215366; PIDN:AAA32302.1; PID:g215370

Query Match          9.2%; Score 45.5; DB 2; Length 69;
Best Local Similarity 22.2%; Pred. No. 2.9e+02;
Matches 12; Conservative 16; Mismatches 21; Indels 5; Gaps 2;

QY 44 MSLLEQSHSP--SLYLQCLSQKLRQERTIPGSGITESKDMHFSLSGLCILLDV 95
Db 17 LELVNQTYSDNVISAYTECFSEVIFVKQVDFV---INESRHIFVEVIGCTYINI 67

RESULT 15
AC1869
hypothetical protein asr0500 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A>Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AC1869
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A>Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anat
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AC1869
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-58 <KUR>
A:Cross-references: UNIPROT:Q8YZG0; GB:BA000019; PIDN:BA072458.1; PID:g17129845; GSPDB:IG
A:Experimental source: strain PCC 7120
C:Genetic:
A:Gene: asr0500

Query Match          9.0%; Score 44.5; DB 2; Length 58;
Best Local Similarity 52.0%; Pred. No. 3.1e+02;
Matches 13; Conservative 3; Mismatches 8; Indels 1; Gaps 1;

QY 45 SLLEQ-SHSPSLYLQCLSQKLRQE 68
Db 13 SLLEQLSVTEQQEILQYLSQLHSQ 37

Search completed: June 20, 2005, 14:03:57
Job time : 40 secs
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2005, 13:45:42 ; Search time 172 Seconds
(without alignments)
285.812 Million cell updates/sec

Title: US-10-713-208-6_COPY_253_348

Perfect score: 497

Sequence: 1 LEDSSLLEVDGPAMKNVEFK.....ITSEKDMHFSSGLCILLDVL 96

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 234051

Minimum DB seq length: 0

Maximum DB seq length: 96

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
1	58	11.7	62	2	Q8VAX8	Q8vax8 white spot
2	57.5	11.6	91	2	Q8W459	Q8w459 arabidopsis
3	55.5	11.2	93	2	Q8ECX4	Q8ecx4 shewanella
4	55	11.1	78	2	Q7U750	Q7u750 synchococc
5	54	10.9	92	1	Y614 PASMU	Y614 PASMU
6	53	10.7	65	2	Q9ZG19	Q9zg19 pasteurella
7	51	10.3	64	2	Q7R2F1	Q7r2f1 giardia lam
8	50.5	10.2	64	2	Q42305	Q42305 arabidopsis
9	50	10.1	90	2	Q7YR94	Q7yr94 bos taurus
10	50	10.1	92	2	Q8TQY7	Q8tqy7 desulfohalob
11	49.5	10.0	67	2	Q72DB9	Q72db9 desulfovibr
12	49.5	10.0	69	2	Q6I6M3	Q6i6m3 sarcophaga
13	49.5	10.0	71	2	Q7T5T2	Q7t5t2 canine coro
14	49.5	10.0	94	2	Q9BF04	Q9bf04 tapirus ind
15	49.5	10.0	96	2	Q84NC6	Q84nc6 oryza sativ
16	49	9.9	63	2	Q6PZM3	Q6pzm3 human immun
17	49	9.9	63	2	Q6PZM4	Q6pzm4 human immun
18	49	9.9	74	2	Q8ZSF6	Q8zsf6 anabaena sp
19	49	9.9	92	2	Q8DUM3	Q8dum3 streptococc
20	48.5	9.8	68	2	Q8YSZ0	Q8ysz0 anabaena sp
21	48.5	9.8	74	2	Q95LE1	Q95le1 canis fami
22	48.5	9.8	75	2	Q9UBA7	Q9uba7 homo sapien
23	48.5	9.8	87	2	Q98672	Q98672 simian cyto
24	48.5	9.8	94	2	Q9BF05	Q9bf05 ceratotheri
25	48.5	9.8	95	2	Q6R4R2	Q6r4r2 brassica ol
26	48.5	9.8	95	2	Q6R4R3	Q6r4r3 brassica ol
27	48.5	9.8	95	2	Q6R4S0	Q6r4s0 brassica ol
28	48.5	9.8	95	2	Q6R4S2	Q6r4s2 brassica ol
29	48.5	9.8	95	2	Q6R4S4	Q6r4s4 brassica ra
30	48.5	9.8	95	2	Q6R4S5	Q6r4s5 brassica ra
31	48.5	9.8	96	2	Q89D25	Q89yd2 bradyrhizob

32	48	9.7	51	2	Q9PDL5	Q9pdl5 xylella fas
33	48	9.7	54	2	Q7MQ15	Q7mq15 vibrio vuln
34	48	9.7	77	2	Q726J2	Q726j2 desulfovibr
35	48	9.7	87	2	Q6Z187	Q6z187 oryza sativ
36	47.5	9.6	59	2	Q9Y8C3	Q9y8c3 coprinus ci
37	47.5	9.6	60	1	HXB1 BRARE	HXB1 brachydanio
38	47.5	9.6	65	1	IACA_PIG	IACA pig
39	47.5	9.6	70	2	Q69TY7	Q69ty7 oryza sativ
40	47.5	9.6	83	2	Q8KK21	Q8kk21 proteus vul
41	47.5	9.6	85	2	Q9C676	Q9c676 arabidopsis
42	47.5	9.6	95	2	Q6XQA3	Q6xqa3 enterobacte
43	47	9.5	58	2	Q9P148	Q9p148 homo sapien
44	47	9.5	62	2	Q73D66	Q73d66 bacillus ce
45	47	9.5	64	2	Q7VAA8	Q7vaa8 prochloroco

ALIGNMENTS

RESULT 1

Q8VAX8	PRELIMINARY;	PRT;	62 AA.
ID	Q8VAX8		
AC	Q8VAX8;		
DT	01-MAR-2002 (Tremblrel. 20, Created)		
DT	01-MAR-2002 (Tremblrel. 20, Last sequence update)		
DT	05-JUL-2004 (Tremblrel. 27, Last annotation update)		
DE	Wav241 (WSSV297).		
OS	White spot syndrome virus (WSSV).		
OC	Viruses; dsDNA viruses, no RNA stage; Nimaviridae; Whispovirus.		
OX	NCBI_TaxID=92652;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=21548311; PubMed=11689662;		
RX	DOI=10.1128/JVI.75.23.11811-11820.2001;		
RA	Yang F., He J., Lin X., Li Q., Pan D., Zhang X., Xu X.;		
RT	"Complete genome sequence of the shrimp white spot bacilliform		
RT	virus.";		
RL	J. Virol. 75:11811-11820(2001).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=20517548; PubMed=11062040; DOI=10.1006/viro.2000.0597;		
RX	DOI=10.1128/JVI.75.23.11811-11820.2001;		
RA	Tsai M.F., Yu H.T., Tzeng H.F., Leu J.H., Chou C.M., Huang C.J.,		
RA	Wang C.H., Lin J.Y., Kou G.H., Lo C.F.;		
RT	"Identification and characterization of a shrimp white spot syndrome		
RT	virus (WSSV) gene that encodes a novel chimeric polypeptide of		
RL	cellular-type thymidine kinase and thymidylate kinase.";		
RN	Virology 277:100-110(2000).		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=21844071; PubMed=11853398; DOI=10.1006/viro.2001.1273;		
RA	Chen L.L., Leu J.H., Huang C.J., Chou C.M., Chen S.M., Wang C.H.,		
RA	Lo C.F., Kou G.H.;		
RT	"Identification of a nucleocapsid protein (VP35) gene of shrimp white		
RT	spot syndrome virus and characterization of the motif important for		
RL	targeting VP35 to the nuclei of transfected insect cells.";		
RN	Virology 293:44-53(2002).		
RP	SEQUENCE FROM N.A.		
RA	Lo C.-F., Kou G.-H.;		
RL	Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF332093; AAL3245.1; -.		
DR	EMBL; AF440570; AAL89165.1; -.		
SQ	SEQUENCE 62 AA; 6698 MW; 9BBCCD06C5367855 CRC64;		

Query Match 11.7%; Score 58; DB 2; Length 62;

Best Local Similarity 31.8%; Pred. No. 48;

Matches 21; Conservative 5; Mismatches 18; Indels 22; Gaps 4;

QY 21 AOKRGCLTVHREADFFWLSLCTADMSLLEQSHSSPSLYLQCLS-----QKLRQERGTI-PG 74

Db 8 ADKRGITIKHMS-----WHLVADIS-----RECCSLFTTTAKQSSGTTSPG 51

QY 75 SGITES 80

[illegible]


```
DR EMBL; AEO06098; AAK02698.1; --
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 92 AA; 10340 MW; 304338CE07ECA377 CRC64;

Query Match
Best Local Similarity 10.9%; Score 54; DB 1; Length 92;
Matches 26; Conservative 16; Mismatches 33; Indels 24; Gaps 4;

QY 2 EDSLLVDPKAMNVEFAKQKGLCTVHREADFFWSLCTAD-MSLLEQSHSP-----SLY 57
DB 7 QEKELMKGDALRMKLYAQSKPKQVTPH-----FTPADSLSMIASSLNQPVVRSLSA 58
QY 58 LQCLSKLQRCQRTIFGSGITESKDMHFSGLGCLLDVL 96
DB 59 VSLLSKKL-----LSSKFLTYSALGMIALYLL 85

RESULT 6
Q9ZG19 PRELIMINARY; PRT; 65 AA.
AC Q9ZG19
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Dihydrofolate reductase/thymidylate synthase (Fragment).
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=L2 434B;
RA Wang L., Steenburg S.D., Zheng Y., Larsen S.H.;
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF087357; AAD04129.1; --
DR MEROPS; M03.007; --
DR GO; GO:004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001567; Pept_M3A_M3B.
DR Pfam; PF01432; Peptidase_M3; 1.
FT NON_TER 1
FT NON_TER 65
SQ SEQUENCE 65 AA; 7640 MW; C8F2D8FF255E63B8 CRC64;

Query Match
Best Local Similarity 10.7%; Score 53; DB 2; Length 65;
Matches 11; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 36 FWSLCTADMSLLEQSHSPSLYLQCLSKLQ 67
DB 3 FWGSLRKSHPSLHALASLYMQSTDRELK 34

RESULT 7
Q7R2F1 PRELIMINARY; PRT; 64 AA.
AC Q7R2F1
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE GLP 623 54983 54789.
OS Giardia lamblia ATCC 50803.
OC Eukaryota; Diplomonadida; Hexamitidae; Giardia.
OX NCBI_TaxID=184922;
RN [1]
RP SEQUENCE OF 61-65 FROM N.A.
RC STRAIN=WB C6;
RX MEDLINE=20370943; PubMed=10908635;
RA Wu G., McArthur A.G., Fiser A., Sali A., Sogin M.L., Miller M.;
RT "Core histones of the amitochondriate protist, Giardia lamblia.";
RL Mol. Biol. Evol. 17:1156-1163 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=WB C6;

DR Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
Olsen G.J., Sogin M.L.;
RT "Draft sequence of the Giardia lamblia genome.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC !- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
DR EMBL; AACB0100021; EAA41517.1; --
SQ SEQUENCE 64 AA; 7813 MW; 1F2077C5421D1FCE CRC64;

Query Match
Best Local Similarity 10.3%; Score 51; DB 2; Length 64;
Matches 8; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 30 HREADFFWSLCTADMSLLEQ 49
DB 10 HAQNOFFWSFCLQKVLAEE 29

RESULT 8
Q42305 PRELIMINARY; PRT; 64 AA.
AC Q42305
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Glycoprotein Epi - carrot (Fragment).
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cell suspension culture of ecotype columbia;
RA CNRS;
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Cell suspension culture of ecotype columbia;
RA Bardet C., Dabos P., Tremouaygue D., Lescure B.;
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z35737; CAA84803.1; --
FT NON_TER 1
FT NON_TER 64
SQ SEQUENCE 64 AA; 7730 MW; 6129171A1B5F27EE CRC64;

Query Match
Best Local Similarity 10.2%; Score 50.5; DB 2; Length 64;
Matches 12; Conservative 9; Mismatches 13; Indels 1; Gaps 1;

QY 38 SLCTADMSLLEQSHSPSLYLQCLSKLQ 72
DB 22 SFCSTPFQLLFY-NITPSVYLALRVGLARDESTM 55

RESULT 9
Q7YR94 PRELIMINARY; PRT; 90 AA.
AC Q7YR94
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Sutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC PubMed=14667821; DOI=10.1016/S0888-7543 (03) 00238-6;
RA Winter A., Alzinger A., Fries R.;
```

[illegible]

Best Local Similarity 24.6%; Pred. No. 7.9e+02;
Matches 17; Conservative 12; Mismatches 19; Indels 21; Gaps 4;

RESULT 13
Q776T2 PRELIMINARY; PRT; 71 AA.
AC Q776T2; (TREMELrel. 25, Created)
DT 01-OCT-2003 (TREMELrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE Non-structural protein 3a.
DE Name=nsp 3a;
GN Canine coronavirus
OS Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus; Group 1 species.
OC NCBI_TaxID=11153;
OX [1]
RN SEQUENCE FROM N.A.
RC STRAIN=EGF10;
RC PubMed=15177899; DOI=10.1016/j.virusres.2004.02.038;
RX Sanchez-Morgado J.M., Poymer S., Morris T.H.;
RT "Molecular characterization of a virulent canine coronavirus BGF
RT strain";
RL Virus Res. 104:27-31(2004).
RL EMBL; AY342160; RAQ17221.1;
DR InterPro; IPR006784; Corona_3.
DR Pfam; PF04694; Corona 3; 1.
SQ SEQUENCE 71 AA; 7706 MW; F89CAA3C72D134D CRC64;

Query Match 10.0%; Score 49.5; DB 2; Length 71;
Best Local Similarity 26.6%; Pred. No. 5.6e+02;
Matches 17; Conservative 18; Mismatches 24; Indels 5; Gaps 2;

QY 34 DFFWLSCTADMSLLBQ---SHSPSLYLQCLSLQRLRGRTIPSGIGTESKDMHFSLGC 90
DB 2 DIVKSIDTSVDALDFEFCAPHTLVKVEFKTLVLCIGF--GDTILEAKKAYAKLGC 59
QY 91 ILLD 94
DB 60 SIIE 63

RESULT 14
Q9BF04 PRELIMINARY; PRT; 94 AA.
AC Q9BF04;
DT 01-JUN-2001 (TREMELrel. 17, Created)
DT 01-JUN-2001 (TREMELrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Prepronociceptin (Fragment).
GN Name=PNOC;
OS Tapirus indicus (Asiatic tapir) (Malayan tapir).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Tapiridae; Tapirus.
OC NCBI_TaxID=9802;
OX [1]
RN SEQUENCE FROM N.A.
RC MEDLINE=21082082; PubMed=11214319; DOI=10.1038/35054550;
RX Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA O'Brien S.J.;
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
RL EMBL; AY011857; AAG38306.1;
DR GO; GO:0007218; P:neuropeptide signaling pathway; IEA.
DR GO; GO:0007268; P:synaptic transmission; IEA.
DR InterPro; IPR002367; Nociceptin.
DR InterPro; IPR006023; Opioid neuropep.
DR Pfam; PF01160; Opioids neuropep; 2.
DR PRINTS; PR01031; ORPHNPRCSR.
FT NON_TER 1 1
FT 94
SQ SEQUENCE 94 AA; 10441 MW; 8FF1A35616592845 CRC64;

Query Match 10.0%; Score 49.5; DB 2; Length 94;

Best Local Similarity 24.6%; Pred. No. 7.9e+02;
Matches 17; Conservative 12; Mismatches 19; Indels 21; Gaps 4;

RESULT 15
Q84NC6 PRELIMINARY; PRT; 96 AA.
AC Q84NC6;
DT 01-JUN-2003 (TREMELrel. 24, Created)
DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Transcription factor MADS23.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Specmatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee S., Kim J., An G.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- SIMILARITY: Contains 1 MADS-box domain.
DR EMBL; AY177694; AAO47704.1;
DR HSSP; Q02078; 1EGW.
DR Gramene; Q84NC6;
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR002100; TF MADSbox.
DR Pfam; PF00319; SRF-TF; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS00666; MADS_BOX_2; 1.
KW DNA-binding; Nuclear protein; Transcription; Transcription regulation.
SQ SEQUENCE 96 AA; 10658 MW; A4C219A3EFE19B6 CRC64;

Query Match 10.0%; Score 49.5; DB 2; Length 96;
Best Local Similarity 31.1%; Pred. No. 8.1e+02;
Matches 14; Conservative 7; Mismatches 21; Indels 3; Gaps 1;

QY 9 VDPGAKNVFKAQKRGICTVHREADFFWSLCTADMSLLSEQSHS 53
DB 11 IDNATSRQVTFKRSGLFKKARELSI---LCDAEVGLLVFSST 52

Search completed: June 20, 2005, 14:03:13
Job time : 174 secs

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OM protein - protein search, using sw model

Run on: June 20, 2005, 13:44:57 ; Search time 158 Seconds
(without alignments)
234.994 Million cell updates/sec

Title: US-10-713-208-6_COPY_253_348
Perfect score: 497
Sequence: 1 LEDSSLEVDGPAKKNVEFK.....ITKDMHFSSLCILLDVL 96

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 115283

Minimum DB seq length: 0
Maximum DB seq length: 96

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : 1: Geneseq_16Dec04:*
2: Geneseqp1980s:*
3: Geneseqp1990s:*
4: Geneseqp2000s:*
5: Geneseqp2001s:*
6: Geneseqp2002s:*
7: Geneseqp2003as:*
8: Geneseqp2003bs:*
9: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	353	71.0	76	4	AAU59349 Peptide #
2	353	71.0	76	4	ABM5868 Peptide #
3	353	71.0	76	4	ABP26511 Peptide #
4	353	71.0	76	4	AAU51869 Peptide #
5	353	71.0	76	4	ABM48388 Peptide #
6	353	71.0	76	4	ABG03427 Peptide #
7	353	71.0	76	4	ABP30341 Peptide #
8	353	71.0	76	4	ABG03792 Peptide #
9	353	71.0	76	4	ABG14805 Peptide #
10	353	71.0	76	4	ABG03922 Peptide #
11	60	12.1	92	3	ABJ05481 Peptide #
12	58	11.7	71	3	ABG0552 Peptide #
13	58	11.7	72	3	ABG6185 Peptide #
14	57.5	11.6	64	4	AAU50887 Peptide #
15	57.5	11.6	78	3	AAU51267 Peptide #
16	57	11.5	73	8	ADG91199 c-Jun hom
17	57	11.5	83	8	ADG91199 c-Jun hom
18	57	11.5	89	2	AAU52628 Peptide #
19	57	11.5	89	3	AAU78548 Peptide #
20	57	11.5	89	5	ABG93398 Peptide #
21	57	11.5	89	5	AAU73195 Peptide #
22	56	11.3	86	5	AAU57011 Peptide #
23	55.5	11.2	68	6	ABJ19123 Peptide #
24	55	11.1	75	5	ABP07109 Peptide #
25	55	11.1	77	6	ADB06692 Peptide #

26	54	10.9	80	4	AAU59349	AAU59349 Propionib
27	54	10.9	80	6	ABM5868	ABM5868 Propionib
28	52.5	10.6	33	5	ABP26511	ABP26511 Streptoco
29	52.5	10.6	56	4	AAU51869	AAU51869 Propionib
30	52.5	10.6	56	6	ABM48388	ABM48388 Propionib
31	52.5	10.6	70	4	ABG03427	ABG03427 Novel hum
32	52	10.5	63	8	ADP30341	ADP30341 Human sec
33	52	10.5	80	4	ABG03792	ABG03792 Novel hum
34	52	10.5	95	4	ABG14805	ABG14805 Novel hum
35	52	10.5	95	4	ABG03922	ABG03922 Novel hum
36	51.5	10.4	41	5	ABJ05481	ABJ05481 Human bre
37	51.5	10.4	67	5	ADK34295	ADK34295 Novel hum
38	51.5	10.4	78	7	ADD44488	ADD44488 Polypepti
39	51	10.3	47	6	ABO13991	ABO13991 Novel hum
40	51	10.3	47	8	ADN60688	ADN60688 Human sec
41	51	10.3	48	2	AAU27586	AAU27586 Human sec
42	51	10.3	48	8	ADG78397	ADG78397 Human sec
43	51	10.3	50	2	AAW58844	AAW58844 Human AX9
44	51	10.3	58	4	AAU55575	AAU55575 Propionib
45	51	10.3	58	6	ABM52094	ABM52094 Propionib

ALIGNMENTS

RESULT 1
AAU515359
ID AAU515359 standard; protein; 76 AA.
XX
AC AAU515359;
XX
DT 12-OCT-2001 (first entry)
XX
DE DE
XX
KW Peptide #1793 encoded by probe for measuring cervical gene expression.
XX
KW Probe; human; microarray; gene expression; cervical epithelial cell;
XX
KW cervical cancer.
XX
OS Homo sapiens.
XX
PN WO200157278-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000670.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488901/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
XX
PT gene expression in human cervical epithelial cells.
XX
PS Claim 27; SEQ ID NO 20185; 487pp; English.
XX
CC The present invention relates to human single exon nucleic acid probes
XX
CC (SEN: see AAI10088-AAI28459). The present sequence is a peptide encoded
XX
CC by one such probe. The SENPs are derived from human Hela cells. The SENPs
XX
CC can be used to produce a single exon microarray, which can be used for
XX
CC measuring human gene expression in a sample derived from human cervical
XX
CC epithelial cells. By measuring gene expression, the probes are therefore
XX
CC useful in grading and/or staging of diseases of the cervix, notably
XX
CC cervical cancer. Note: The sequence data for this patent did not form

CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 76 AA;

Query Match 71.0%; Score 353; DB 4; Length 76;
Best Local Similarity 100.0%; Pred. No. 6.7e-36;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEDSSILLEVDGPMKNVFKAKRGICTVHREADFFWSLCTADMSLLEQSHSPSLYLQC 60
DB 9 LEDSSILLEVDGPMKNVFKAKRGICTVHREADFFWSLCTADMSLLEQSHSPSLYLQC 68
QY 61 LSQKLQRE 68
DB 69 LSQKLQRE 76

RESULT 2
ABB34356
ID ABB34356 standard; peptide; 76 AA.
XX
AC ABB34356;
XX
DT 04-FEB-2002 (first entry)
XX
DE Peptide #1862 encoded by human foetal liver single exon probe.
XX
KW Human, foetal liver; gene expression; single exon nucleic acid probe.
XX
OS Homo sapiens.
XX
PN WO200157277-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000669.
XX
PR 04-FEB-2000; 2000US-0180312P.
XX
PR 26-MAY-2000; 2000US-0207456P.
XX
PR 30-JUN-2000; 2000US-00608408.
XX
PR 03-AUG-2000; 2000US-00632366.
XX
PR 21-SEP-2000; 2000US-0234687P.
XX
PR 27-SEP-2000; 2000US-0236359P.
XX
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-483447/52.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human fetal liver.
XX
PS Claim 27; SEQ ID NO 26991; 639pp + Sequence Listing; English.
XX
XX

CC The invention relates to a single exon nucleic acid probe for measuring
CC human gene expression in a sample derived from human foetal liver. The
CC single exon nucleic acid probes may be used for predicting, measuring and
CC displaying gene expression in samples derived from human fetal liver. The
CC present invention is a peptide encoded by a single exon nucleic acid probe
CC of the invention. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 76 AA;

Query Match 71.0%; Score 353; DB 4; Length 76;
Best Local Similarity 100.0%; Pred. No. 6.7e-36;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEDSSILLEVDGPMKNVFKAKRGICTVHREADFFWSLCTADMSLLEQSHSPSLYLQC 60
DB 9 LEDSSILLEVDGPMKNVFKAKRGICTVHREADFFWSLCTADMSLLEQSHSPSLYLQC 68
QY 61 LSQKLQRE 68
DB 69 LSQKLQRE 76

RESULT 4
ABB29199
ID ABB29199 standard; peptide; 76 AA.

DB 9 LEDSSILLEVDGPMKNVFKAKRGICTVHREADFFWSLCTADMSLLEQSHSPSLYLQC 68
QY 61 LSQKLQRE 68
DB 69 LSQKLQRE 76
RESULT 3
AAM27837
ID AAM27837 standard; protein; 76 AA.
XX
AC AAM27837;
XX
DT 17-OCT-2001 (first entry)
XX
DE Peptide #1874 encoded by probe for measuring placental gene expression.
XX
KW Probe; microarray; human; placenta; antenatal diagnosis;
XX
OS Homo sapiens.
XX
PN WO200157272-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000663.
XX
PR 04-FEB-2000; 2000US-0180312P.
XX
PR 26-MAY-2000; 2000US-0207456P.
XX
PR 30-JUN-2000; 2000US-00608408.
XX
PR 03-AUG-2000; 2000US-00632366.
XX
PR 21-SEP-2000; 2000US-0234687P.
XX
PR 27-SEP-2000; 2000US-0236359P.
XX
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488897/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human placenta.
XX
PS Claim 27; SEQ ID NO 28106; 654pp; English.
XX
XX

CC The present invention relates to single exon nucleic acid probes (SNP:
CC see AAI31315-AAI57546). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for producing a microarray for
CC predicting, measuring and displaying gene expression in samples derived
CC from human placenta. The probes are useful for antenatal diagnosis of
CC human genetic disorders
XX
SQ Sequence 76 AA;

Query Match 71.0%; Score 353; DB 4; Length 76;
Best Local Similarity 100.0%; Pred. No. 6.7e-36;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEDSSILLEVDGPMKNVFKAKRGICTVHREADFFWSLCTADMSLLEQSHSPSLYLQC 60
DB 9 LEDSSILLEVDGPMKNVFKAKRGICTVHREADFFWSLCTADMSLLEQSHSPSLYLQC 68
QY 61 LSQKLQRE 68
DB 69 LSQKLQRE 76

RESULT 4
ABB29199
ID ABB29199 standard; peptide; 76 AA.

XX ABB29199;
AC
XX
DT 01-FEB-2002 (first entry)
XX
DE Peptide #1850 encoded by breast cell single exon nucleic acid probe.
XX
KW Human; microarray; single exon probe; gene expression; breast; disease;
KW Cancer.
OS Homo sapiens.
XX
PN WO200157271-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US0000662.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-496933/54.
XX
PT New spatially-addressable set of single exon nucleic acid probes, useful
PT for measuring gene expression in sample derived from human breast,
PT comprises number of single exon nucleic acid probes.
XX
PS Claim 27; SEQ ID NO 12167; 327pp + Sequence Listing; English.
XX
CC The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human breast and BT 474 cells. The method involves contacting the
CC probes with a collection of detectably labelled nucleic acids derived
CC from mRNA of human breast, and then measuring the label bound to each
CC probe of the microarray. The probes are useful for verifying the
CC expression of regions of genomic DNA predicted to encode proteins. They
CC are useful for gene discovery, and for determining predisposition and/or
CC prognosing breast disease. Gene expression analysis is useful for
CC assessing the toxicity of chemical agents on cells. The microarray of
CC this invention presents a far greater diversity of probes for measuring
CC gene expression, with far less bias than expressed sequence tag
CC microarrays. The method is suitable for rapid production of functional
CC information from genomic sequence. The present sequence is a peptide
CC encoded by a single exon nucleic acid probe of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 76 AA;

Query Match 71.0%; Score 353; DB 4; Length 76;
Best Local Similarity 100.0%; Pred. No. 6.7e-36;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEDSSLEVDGPAMKNVEFKAKRGCTVHREADFFWSLCTADMSLLEQSHSPSLYLQC 60
DB 9 LEDSSLEVDGPAMKNVEFKAKRGCTVHREADFFWSLCTADMSLLEQSHSPSLYLQC 68
QY 61 LSQKLQRE 68
DB 69 LSQKLQRE 76

RESULT 5

ABB19775
ID ABB19775 standard; protein; 76 AA.
XX
AC ABB19775;
XX
DT 23-JAN-2002 (first entry)
XX
DE Protein #1774 encoded by probe for measuring heart cell gene expression.
XX
KW Human; gene expression; heart; microarray; vascular system;
KW cardiovascular disease; hypertension; cardiac arrhythmia;
KW congenital heart disease.
XX
OS Homo sapiens.
XX
PN WO200157274-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US0000666.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488899/53.
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
PT hearts.
XX
PS Claim 15; SEQ ID NO 21545; 530pp; English.
XX
CC The present invention relates to single exon nucleic acid probes for
CC measuring human gene expression in a sample derived from human heart (see
CC ABA21535-ABA41305). The present sequence is a protein encoded by one such
CC probe. The probes may be used for predicting, measuring and displaying
CC gene expression in samples derived from the human heart via microarrays.
CC By measuring gene expression, the probes are useful for predicting,
CC diagnosing, grading, staging, monitoring and prognosing diseases of the
CC human heart and vascular system e.g. cardiovascular disease,
CC hypertension, cardiac arrhythmias and congenital heart disease. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 76 AA;

Query Match 71.0%; Score 353; DB 4; Length 76;
Best Local Similarity 100.0%; Pred. No. 6.7e-36;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEDSSLEVDGPAMKNVEFKAKRGCTVHREADFFWSLCTADMSLLEQSHSPSLYLQC 60
DB 9 LEDSSLEVDGPAMKNVEFKAKRGCTVHREADFFWSLCTADMSLLEQSHSPSLYLQC 68
QY 61 LSQKLQRE 68
DB 69 LSQKLQRE 76

RESULT 6
AAM67546
ID AAM67546 standard; protein; 76 AA.
XX
AC AAM67546;

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XX DT 06-NOV-2001 (first entry)
XX DE Human bone marrow expressed probe encoded protein SEQ ID NO: 27852.
XX KW Human; bone marrow expressed exon; gene expression analysis; probe;
XX KW microarray; cancer; leukaemia; lymphoma; myeloma.
XX OS Homo sapiens.
XX PN WO200157276-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000668.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX XX WPI; 2001-488900/53.
XX DR Human genome-derived single exon nucleic acid probes useful for analyzing
XX PT gene expression in human bone marrow.
XX PT gene expression in human bone marrow.
XX PS Example 4; SEQ ID NO 27852; 658pp + Sequence Listing; English.
XX XX
XX CC The present invention provides a number of single exon nucleic acid
XX CC probes which are derived from genomic sequences expressed in the human
XX CC bone marrow. They can be used to measure gene expression in bone marrow
XX CC samples, which may enable the improved diagnosis and treatment of cancers
XX CC such as lymphoma, leukaemia and myeloma. The present sequence is a
XX CC protein encoded by one of the probes of the invention
XX SQ Sequence 76 AA;
XX
Query Match 71.0%; Score 353; DB 4; Length 76;
Best Local Similarity 100.0%; Pred. No. 6.7e-36;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LEDSSILLEVDGPAMKNVFKAKRGICTVHREADFFWSLCTADMSLLEQSHSPSLYLQC 60
DB 9 LEDSSILLEVDGPAMKNVFKAKRGICTVHREADFFWSLCTADMSLLEQSHSPSLYLQC 68
QY 61 LSQKLQKE 68
DB 69 LSQKLQKE 76
XX
RESULT 7
AAM55153
ID AAM55153 standard; protein; 76 AA.
XX AC AAM55153;
XX DT 05-NOV-2001 (first entry)
XX DE Human brain expressed single exon probe encoded protein SEQ ID NO: 27258.
XX KW Human; brain expressed exon; gene expression analysis; probe; microarray;
XX KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
XX OS Homo sapiens.
XX PN WO200157275-A2.

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XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000667.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX XX WPI; 2001-483446/52.
XX DR Single exon nucleic acid probes for analyzing gene expression in human
XX PT brains.
XX PT brains.
XX PS Example 4; SEQ ID NO 27258; 650pp + Sequence Listing; English.
XX XX
XX CC The present invention provides a number of single exon nucleic acid
XX CC probes which are derived from genomic sequences expressed in the human
XX CC brain. They can be used to measure gene expression in brain cell samples,
XX CC which may enable the diagnosis and improved treatment of nervous system
XX CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
XX CC epilepsy and cancers. The present sequence is a protein encoded by one of
XX CC the probes of the invention
XX SQ Sequence 76 AA;
XX
Query Match 71.0%; Score 353; DB 4; Length 76;
Best Local Similarity 100.0%; Pred. No. 6.7e-36;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LEDSSILLEVDGPAMKNVFKAKRGICTVHREADFFWSLCTADMSLLEQSHSPSLYLQC 60
DB 9 LEDSSILLEVDGPAMKNVFKAKRGICTVHREADFFWSLCTADMSLLEQSHSPSLYLQC 68
QY 61 LSQKLQKE 68
DB 69 LSQKLQKE 76
XX
RESULT 8
ABG49189
ID ABG49189 standard; peptide; 76 AA.
XX AC ABG49189;
XX DT 25-FEB-2003 (first entry)
XX DE Human liver peptide, SEQ ID No 27837.
XX KW Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
XX KW hypercholesterolaemia; coronary heart disease.
XX OS Homo sapiens.
XX PN WO200157273-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000664.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 21-SEP-2000; 2000US-00632366.
XX PR 03-AUG-2000; 2000US-0234687P.

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PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
PA Penn SG, Hanzel DK, Chen W, Rank DR;
PI WPI; 2001-488898/53.
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human adult liver.
PT Claim 27; SEQ ID NO 27837; 658pp; English.
XX The invention relates to a single exon nucleic acid probe (SENP) (I) for
CC measuring human gene expression in a sample derived from human adult
CC liver, comprising one of 13109 defined nucleotide sequences given in the
CC specification (or complements/ fragments). The probe hybridizes at high
CC stringency to a nucleic acid molecule expressed in the human adult liver.
CC (I) may be used for predicting, measuring and displaying gene expression
CC in samples derived from human adult liver. The genes identified may be
CC involved in genetic liver diseases such as cirrhosis,
CC hyperlipoproteinemia, hyperlipidaemia and hypercholesterolaemia which is
CC associated with coronary heart disease. ABG47348-ABG59930 represent human
CC liver single exon encoded peptides of the invention. Note: The sequence
CC information for this patent does not appear in the printed specification
CC but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX Sequence 76 AA;
SQ Query Match 71.0%; Score 353; DB 4; Length 76;
Best Local Similarity 100.0%; Pred. No. 6.7e-36;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LEDSSILLEVDGPAKKNVEPKAQRGLCTVHREADFFWSLCTADMSLLEQSHSPSYLQC 60
DB 9 LEDSSILLEVDGPAKKNVEPKAQRGLCTVHREADFFWSLCTADMSLLEQSHSPSYLQC 68
QY 61 LSQKLRLQE 68
DB 69 LSQKLRLQE 76
RESULT 9
AAM03118
ID AAM03118 standard; protein; 76 AA.
XX AAM03118;
AC AAM03118;
XX 09-OCT-2001 (first entry)
DT Peptide #1800 encoded by probe for measuring breast gene expression.
DE Probe; human; breast disease; breast cancer; development disorder;
XX inflammatory disease; proliferative breast disease; non-carcinoma tumour.
KW Homo sapiens.
OS WO200157270-A2.
PN 09-AUG-2001.
PD 29-JAN-2001; 2001WO-US000661.
XX 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX

PA (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-476286/51.
XX Novel single exon nucleic acid probe used to measuring gene expression in
PT a human breast.
XX Claim 27; SEQ ID NO 11858; 322pp; English.
XX The present invention relates to novel single exon nucleic acid probes
CC (see AAI00010-AA110067). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for measuring human gene expression in
CC a human breast sample, where the probe hybridizes at high stringency to a
CC nucleic acid expressed in the human breast. The probes are useful for
CC predicting, diagnosing, grading, staging, monitoring and prognosing
CC diseases of the human breast, particularly those diseases with polygenic
CC aetiology. The diseases include: breast cancer; disorders of development,
CC inflammatory diseases of the breast; fibrocystic changes; proliferative,
CC breast disease and non-carcinoma tumours. Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX Sequence 76 AA;
SQ Query Match 71.0%; Score 353; DB 4; Length 76;
Best Local Similarity 100.0%; Pred. No. 6.7e-36;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LEDSSILLEVDGPAKKNVEPKAQRGLCTVHREADFFWSLCTADMSLLEQSHSPSYLQC 60
DB 9 LEDSSILLEVDGPAKKNVEPKAQRGLCTVHREADFFWSLCTADMSLLEQSHSPSYLQC 68
QY 61 LSQKLRLQE 68
DB 69 LSQKLRLQE 76
RESULT 10
ABG37140
ID ABG37140 standard; peptide; 76 AA.
XX ABG37140;
AC ABG37140;
XX 19-AUG-2002 (first entry)
DT Human peptide encoded by genome-derived single exon probe SEQ ID 26805.
DE Human; single exon probe; asthma; lung cancer; COPD; ILD;
XX chronic obstructive pulmonary disease; interstitial lung disease;
KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
KW tuberosus sclerosis; Gaucher's disease; Niemann-Pick disease;
KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
KW primary ciliary dyskinesia; pulmonary hypertension;
KW hyaline membrane disease.
XX Homo sapiens.
OS WO200186003-A2.
PN 15-NOV-2001.
PD 30-JAN-2001; 2001WO-US000665.
XX 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX

PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI WPI; 2002-114183/15.
XX Spatially-addressable set of single exon nucleic acid probes, used to
PT measure gene expression in human lung samples.
XX
XX Claim 27; SEQ ID NO 26805; 634pp; English.
XX
XX The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human lung comprising single exon nucleic acid probes having one of
CC 12614 nucleic acid sequences mentioned in the specification, or their
CC complements or the 12387 open reading frames derived from the 12614
CC probes. Also included are a microarray comprising the novel set of probes
CC; the novel set of probes which hybridise at high stringency to a nucleic
CC acid expressed in the human lung; measuring gene expression in a sample
CC derived from human lung, comprising (a) contacting the array with a
CC collection of detectably labeled nucleic acids derived from human lung
CC mRNA, and (b) measuring the label detectably bound to each probe of the
CC array; identifying exons in a eukaryotic genome, comprising (a)
CC algorithmically predicting at least one exon from genomic sequences of
CC the eukaryote; and (b) detecting specific hybridisation of detectably
CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
CC having a fragment identical to the predicted exon, the probe is included
CC in the above mentioned microarray; assigning exons to a single gene,
CC comprising (a) identifying exons from genomic sequence by the method
CC above and (b) measuring the expression of each of the exons in several
CC tissues and/or cell types using hybridisation to a single exon
CC microarrays having a probe with the exon, where a common pattern of
CC expression of the exons in the tissues and/or cell types indicates that
CC the exons should be assigned to a single gene; a peptide comprising one
CC of 12011 sequences, mentioned in the specification, or encoded by the
CC probes/open reading frames (ORF). The probes are used for gene expression
CC analysis, and for identifying exons in a gene, particularly using human
CC lung derived mRNA and for the study of lung diseases such as asthma, lung
CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Heremansky-
CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
CC Kargener syndrome, fibrocystic pulmonary dysplasia, primary ciliary
CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The
CC present sequence is a peptide/protein encoded by a single exon probe of
CC the invention. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 76 AA;
Query Match 71.0%; Score 353; DB 5; Length 76;
Best Local Similarity 100.0%; Pred. No. 6.7e-36;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LEDSSLLLEVDGPAKMKVFEKAKRGICLVHREADPFWSLCTADMSLLLEQSHSPSLYLQCL 60
DB 1 LEDSSLLLEVDGPAKMKVFEKAKRGICLVHREADPFWSLCTADMSLLLEQSHSPSLYLQCL 68
QY 61 LSQKLQKE 68
DB 69 LSQKLQKE 76
RESULT 11
AAB33250
ID AAB33250 standard; protein; 92 AA.
XX
XX AAB33250;
AC

XX 25-JAN-2001 (first entry)
XX Eucalyptus grandis transcription factor protein sequence #407.
XX
XX Plant; transcription factor; gene expression; eucalyptus; pine; acacia;
KW poplar; sweetgum; teak; mahogany; bz1p; G-box binding factor;
KW basic helix-loop-helix zipper; homeotic; homeodomain; homeobox; MADS;
KW homeodomain zipper; LIM domain; AP2; EREBs; zinc finger domain;
KW type 2 Cys2His2; CCAAT box element; MYB.
XX
OS Eucalyptus grandis.
XX
XX WO2000053724-A2.
XX
XX 14-SEP-2000.
XX
XX 09-MAR-2000; 2000WO-US006112.
XX
XX 11-MAR-1999; 99US-00266513.
XX 18-AUG-1999; 99US-0149485P.
XX
XX (GENE-) GENESIS RES & DEV CORP LTD.
XX (FLET-) FLETCHER CHALLENGE FORESTS LTD.
XX
XX Wood M, McGrath A, Shenk MA, Glenn M;
PI WPI; 2000-579369/54.
XX
XX New isolated polynucleotide encoding a plant transcription factor for
PT producing a plant e.g. a woody plant, preferably eucalyptus or pine,
PT having modified gene expression or modified activity of a polypeptide.
XX
XX Claim 8; Page 694; 747pp; English.
XX
XX The present invention relates to novel plant transcription factors from
CC Eucalyptus grandis or Pinus radiata. The present sequence is one such
CC transcription factor. The transcription factor may be used to produce a
CC plant having modified gene expression such as a woody plant e.g. a
CC eucalyptus, pine, acacia, poplar, sweetgum, teak, or mahogany species or
CC to modify the activity of a polypeptide in a plant. The transcription
CC factors of the present invention are members from the following families
CC of regulatory proteins: bz1p, bz1p family of G-box binding factors, basic
CC helix-loop-helix zipper, homeotic/homeodomain/homeobox/MADS, homeodomain
CC zipper, LIM domain, AP2 and EREBs, zinc finger domains of type 2
CC Cys2His2, CCAAT box elements and MYB
XX
SQ Sequence 92 AA;
Query Match 12.1%; Score 60; DB 3; Length 92;
Best Local Similarity 28.4%; Pred. No. 30;
Matches 19; Conservative 17; Mismatches 27; Indels 4; Gaps 2;
QY 2 EDSSLLLEVDGPAKMKVFEKAKRGICLVHREADPFWSLCTADMSLLLEQSHSPSLYLQCL 61
DB 4 EKIKIKIDNLTARQVTFKRRRLI---KKABELSVLCADVSLVFS-ATGKLYDFSS 59
QY 62 SQKLQKE 68
DB 60 SQKMKGE 66
RESULT 12
AAG60552
ID AAG60552 standard; protein; 71 AA.
XX
XX AAG60552;
AC
XX 18-OCT-2000 (first entry)
XX
XX Arabidopsis thaliana protein fragment SEQ ID NO: 78442.
DE Protein identification; signal transduction pathway; metabolic pathway;
XX
KW

KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

XX Arabidopsis thaliana.

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(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-483426/52.

N-PSDB; AAK63668.

Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
useful for preventing, diagnosing and/or treating cancers and metastasis.

Claim 11; SEQ ID NO 18480; 3071pp + Sequence Listing; English.

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OM protein - protein search, using sw model

Run on: June 20, 2005, 14:03:24 ; Search time 157 Seconds
(without alignments)
234.790 Million cell updates/sec

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Gapop 10.0 , Gapext 0.5

Searched: 171042 seqs, 383979560 residues

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22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	353	71.0	76	9	US-09-864-761-35073
2	63	12.7	50	15	US-10-424-599-178808
3	60.5	12.2	86	16	US-10-437-963-140300
4	60	12.1	85	15	US-10-424-599-207479
5	60	12.1	92	16	US-10-856-499-2205
6	58.5	11.8	67	16	US-10-437-963-138338
7	58.5	11.8	87	17	US-10-424-599-208754
8	58.5	11.8	87	17	US-10-732-923-15868
9	58.5	11.8	94	15	US-10-424-599-193827
10	57.5	11.6	86	16	US-10-437-963-191300
11	57	11.5	89	9	US-09-159-469-26

12	57	11.5	89	9	US-09-798-042-26
13	57	11.5	89	9	US-09-953-108-26
14	57	11.5	96	15	US-10-424-599-206718
15	56	11.3	72	17	US-10-732-923-16396
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17	55.5	11.2	68	17	US-10-470-048B-448
18	55	11.1	78	16	US-10-437-963-102975
19	55	11.1	86	17	US-10-732-923-16811
20	54.5	11.0	66	17	US-10-732-923-16612
21	54	10.9	69	16	US-10-425-115-292382
22	54	10.9	75	16	US-10-437-963-104068
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24	53.5	10.8	77	17	US-10-732-923-16413
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26	53	10.7	51	15	US-10-424-599-194305
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30	53	10.7	79	16	US-10-437-963-102725
31	53	10.7	84	15	US-10-424-599-288479
32	52	10.5	45	15	US-10-424-599-225162
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36	52	10.5	68	16	US-10-425-115-247598
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41	52	10.5	91	15	US-10-425-114-57053
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45	51.5	10.4	86	15	US-10-424-599-280476

ALIGNMENTS

RESULT 1

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; Sequence 35073, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wenheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeonica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30

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, PRIOR FILING DATE: 2001-01-30
, PRIORITY APPLICATION NUMBER: US 60/234, 687
, PRIOR FILING DATE: 2000-09-21
, PRIORITY APPLICATION NUMBER: US 09/608, 408
, PRIOR FILING DATE: 2000-06-30
, PRIORITY APPLICATION NUMBER: US 09/774, 203
, PRIOR FILING DATE: 2001-01-29
, NUMBER OF SEQ ID NOS: 49117
, SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
, SEQ ID NO 35073
, LENGTH: 76
, TYPE: PRT
, ORGANISM: Homo sapiens
, FEATURE:
, OTHER INFORMATION: MAP TO AC007283.3
, OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.3
, OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.1
, OTHER INFORMATION: EXPRESSED IN HELI00, SIGNAL = 2.4
, OTHER INFORMATION: EXPRESSED IN HEAT, SIGNAL = 2.7
, OTHER INFORMATION: EXPRESSED IN HEMT, SIGNAL = 3.8
, OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.8
, OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 5.4
, OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.6
, OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 3.6
, OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 5.9
, OTHER INFORMATION: EST_HUMAN HIT: A1139524.1, EVALUATE 2.00e-38
, US-09-864-761-35073

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RESULT 2
US-10-424-599-178808
; Sequence 178808, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 178808
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_132480C.1.pgp
US-10-424-599-178808

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Best Local Similarity 28.1%; Pred. No. 5.7;
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Db 2 FFW-----LQDKYSTSVFYEQ-----RSGLTERSDIHFKNHGM 36

RESULT 3
US-10-437-963-140300
; Sequence 140300, Application US/10437963
; Publication NO. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Bing

```

RESULT 3

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US-10-437-963-140300
; Sequence 140300, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: Thomas J.
; APPLICANT: La Rosa, David K.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 140300
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(86)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_41510C.1.pep
US-10-437-963-140300

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Query Match 12.2%; Score 60.5; DB 16; Length 86;

Best Local Similarity 32.2%; **Pred. No.** 23;
Matches 19; **Conservative** 10; **Mismatches** 23; **Indels** 7; **Gaps** 3;

Qy 25 GLCTVHEADFFWSLCTADMSLLSEQSHSSPSLYIQLCSOKLRQERTIPGSGITESKDM 83
19 GPICRXREDKMGWTGCVA-ARLEAAAPRPS-VLETISRLRRS-----GGDLDQEDDV 70

RESULT 4

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US-10-424-599-207479
; Sequence 207479, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 207479
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_29379C.1.pep
US-10-424-599-207479

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Query Match 12.1%; Score 60; DB 15; Length 85;

Best Local Similarity	31.5%;	Pred. No. 26;	
Matches 23;	Conservative 8;	Mismatches 24;	Indels 18; Gaps 3;
Qy	4	SSILEV-----DGPAMK-----	NVEFKAQKRGCLCTVHREADFFWSLCTADMSLLEQ 49
Db	11	SSLKEIVSNVGEAMKRNHMPYAQQQQQLKQLQCNTRKAGKFI----	TSSNLEED 66
Qy	50	SHSPSPSLYLQCLLS	62
Db	67	GASSASLLLTCTIS	79

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RESULT 5
US-10-856-499-2205
; Sequence 2205, Application US/10856499
; Publication No. US20040259145A1
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Modification of Gene Transcription
; FILE REFERENCE: 11000.1021C2
; CURRENT APPLICATION NUMBER: US/10/856,499
; CURRENT FILING DATE: 2004-05-28
; NUMBER OF SEQ ID NOS: 2370
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2205
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-10-856-499-2205

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Query Match      12.1%; Score 60; DB 16; Length 92;
Best Local Similarity 28.4%; Pred.No. 29;
Matches 19; Conservative 17; Mismatches 27; Indels 4; Gaps 2;
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Qy    2 EDSSLLEVDPGMKNVFEKAKRGCTVTHREADFFWSLCTADMGLSQSHSSPSLYLOCL 61  
| : :: | : ||| : :||| : :||| : :||| : :||| : :||  
Db    4 EKIKIKKIDNLTAHQVFVSKRRRGLI---KKAELSVLCDADVSLIVFS-ATGKLYDFSS 59
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Qy    62 SQKLQRQE 68  
|:::|  
Db   60 SROMKGGE 66
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RESULT 6
US-10-437-963-138338
; Sequence 138338, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 138338
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_39737C.1.1.p
US-10-437-963-138338

OTHER INFORMATION: Clone ID: PAT_MRT4530_39737C.1.pcp
US-10-437-963-138338

Query Match	11.8%	Score 58.5;	DB 16;	Length 67;
Best Local Similarity	26.5%;	Pred. No. 30;		
Matches 13;	Conservative	9;	Mismatches 18;	Indels 9

Qy		20	KAQKRGICTVHREADFWSLCTADMSILLEQSHSSPSIYLQCLSQKLQRE	68
	: :		: : : : : :	
Dδ		8	KNQKETACSI-----LCMIDRKQLQNQH LAVTQYPQCINNTVLQQ	47

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RESULT 7
US-10-424-599-208754
; Sequence 208754, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovacic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 208754
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_30533C.1.pgp
US-10-424-599-208754

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Query Match	11.8%	Score 58.5;	DB 15;	Length 87;
Best Local Similarity	40.5%	Pred. No. 42;		
Matches 15; Conservative	7;	Mismatches 10;	Indels 5;	Gaps 2;

Qy	61	LSQKLRERGTTPGSGITESKDMH--FSSLGCIILDV	95
		: : : : : : : : : : : : : : : : : : : :	
Dd	38	LKKLRLOQAVGGS---EGMDMHTLQSGIEQVILQL	71

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RESULT 8
US-10-732-923-15868
; Sequence 15868, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 15868
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(87)
; OTHER INFORMATION: unsure at all xaa locations
US-10-732-923-15868

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Query Match	11.8%	Score 58.5;	DB 17;	Length 87;
Best Local Similarity	25.8%;	Pred. NO. 42;		
Matches	21;	Conservative 15;	Mismatches 37;	Indels 9; Gaps 2;

Qy	2	EDSSLEVDGPMKNYEFKAQKRGCLGTCVIREADFFWSLCTADMSLEQSHSSPSLYLQCL	61
Db	4	ERREIKRIISAAARQVTFKRRGL-----FKKAELSVLCDADVALVFSGTGK-----L	54


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RESULT 14
US-10-424-599-206718
; Sequence 206718, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Chao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Mo
; TITLE OF INVENTION: Plants and Uses Th

```

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Query Match      11.3%; Score 56; DB 17; Length 72;
Best Local Similarity 24.2%; Pred. No. 67;
Matches 16; Conservative 14; Mismatches 26; Indels 10; Gaps 2;

Qy   5  SILLEVDGPAKNVFEKAAQKGILCTVHREADFFWSLCTADMSLLEQS-----HSGPSLY 57
      ::::|::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db   7  AIRRINDNSTRQVTFSRRNRLLKKARELSI----LCDAEVGLMVFSTGKYDYASTSRF 63
      ::::|::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

Qy   58  LOCLSQ 63
      ||::
      |:::
Db   64  KYCLNR 69
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Search completed: June 20, 2005, 14:16:42
Job time : 161 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 20, 2005, 13:54:53 ; Search time 43 Seconds
(without alignments)
166.658 Million cell updates/sec

Title: US-10-713-208-6_COPY_253_348
Perfect score: 497
Sequence: 1 LEDSSLEVDGPAKKNVEK.....ITESKDMHFSSLCILLDVL 96

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 320760

Minimum DB seq length: 0
Maximum DB seq length: 96

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A COMB pep.*
2: /cgn2_6/ptodata/1/iaa/5B COMB pep.*
3: /cgn2_6/ptodata/1/iaa/6A COMB pep.*
4: /cgn2_6/ptodata/1/iaa/6B COMB pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS COMB pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1 pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60	12.1	92	4	US-09-640-211A-2205
2	57	11.5	89	3	US-08-975-762-26
3	57	11.5	89	3	US-08-921-324-26
4	57	11.5	89	3	US-09-295-028-26
5	57	11.5	89	3	US-09-106-582-26
6	57	11.5	89	4	US-09-159-469-26
7	57	11.5	89	4	US-09-693-542-26
8	55.5	11.2	64	4	US-09-248-796A-25093
9	51.5	10.4	75	4	US-09-621-976-7393
10	50	10.1	47	3	US-09-187-789-52
11	50	10.1	47	4	US-09-139-600-47
12	50	10.1	47	4	US-09-989-903-52
13	50	10.1	88	4	US-09-583-110-4281
14	50	10.1	88	4	US-09-107-433-3932
15	50	10.1	96	4	US-09-107-532A-4733
16	49.5	10.0	63	4	US-09-543-681A-5822
17	49	9.9	80	4	US-09-248-796A-23290
18	49	9.9	82	3	US-08-905-223-481
19	48.5	9.8	96	2	US-08-737-560A-9
20	47.5	9.6	51	3	US-09-052-089A-5
21	47.5	9.6	72	4	US-09-270-767-60440
22	47.5	9.6	86	4	US-09-621-976-4271
23	47.5	9.6	87	4	US-09-270-767-44962
24	47	9.5	61	4	US-09-248-796A-23862
25	47	9.5	78	4	US-09-248-796A-24764
26	47	9.5	88	4	US-09-687-637B-41
27	47	9.5	88	4	US-09-248-796A-25988

ALIGNMENTS

RESULT 1

US-09-640-211A-2205
; Sequence 2205, Application US/09640211A
; Patent No. 6833446

; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; FILE REFERENCE: 11000.1021C1U
; CURRENT APPLICATION NUMBER: US/09/640,211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2205
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Eucalyptus grandis

US-09-640-211A-2205

Query Match 12.1%; Score 60; DB 4; Length 92;
Best Local Similarity 28.4%; Pred. No. 2.8;
Matches 19; Conservative 17; Mismatches 27; Indels 4; Gaps 2;

QY 2 EDSLSLEVDGPAKKNVEFKAQKGLCTVHREADFFWSLCTADMSLLEQSHSSFLYLQCL 61
DB 4 EKIKKIDNLTARQVTFKRRRLI---KKAELSVLCDADVSLIVFS-ATGKLYDFSS 59

QY 62 SQKLRQ 68
DB 60 SRQMKGE 66

RESULT 2

US-08-975-762-26
; Sequence 26, Application US/08975762
; Patent No. 6207169

; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Houghton, Raymond
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington

TREATMEN

/ COUNTRY: USA
/ ZIP: 98104
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/975,762
/ FILING DATE: 21-MAR-1997
/ CLASSIFICATION: 424
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Maki, David J.
/ REGISTRATION NUMBER: 31,392
/ REFERENCE/DOCKET NUMBER: 210121.439
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 206-622-4900
/ TELEFAX: 206-682-6031
/ INFORMATION FOR SEQ ID NO: 26:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 89 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ ORIGINAL SOURCE:
/ ORGANISM: Ehrlichia
/ US-08-975-762-26

Query Match 11.5%; Score 57; DB 3; Length 89;
Best Local Similarity 24.6%; Pred. No. 6.7;
Matches 15; Conservative 9; Mismatches 17; Indels 20; Gaps 2;

QY 33 ADFWLSLCTADMSLLEQSHSPSLYLQCLSQKLQKRGRTIPGSGITESKDMHFSSLGCIL 92
Db 28 SSFFFLYSTTDF-LCTRSHSCPDAY-----VTDKQPQVYAAGCVY 67
QY 93 L 93
Db 68 I 68

RESULT 3
US-08-821-324-26
/ Sequence 26, Application US/08821324
/ Patent No. 6231869
/ GENERAL INFORMATION:
/ APPLICANT: Reed, Steven G.
/ APPLICANT: Lodes, Michael J.
/ APPLICANT: Houghton, Raymond
/ TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND
/ NUMBER OF SEQUENCES: 38
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: SEED and BERRY LLP
/ STREET: 6300 Columbia Center, 701 Fifth Avenue
/ CITY: Seattle
/ STATE: Washington
/ COUNTRY: USA
/ ZIP: 98104
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/821,324
/ FILING DATE: 21-MAR-1997
/ CLASSIFICATION: 424
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Maki, David J.
/ REGISTRATION NUMBER: 31,392
/ REFERENCE/DOCKET NUMBER: 210121.439
/ TELECOMMUNICATION INFORMATION:

/ TELEPHONE: 206-622-4900
/ TELEFAX: 206-682-6031
/ INFORMATION FOR SEQ ID NO: 26:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 89 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ ORIGINAL SOURCE:
/ ORGANISM: Ehrlichia
/ US-08-821-324-26

Query Match 11.5%; Score 57; DB 3; Length 89;
Best Local Similarity 24.6%; Pred. No. 6.7;
Matches 15; Conservative 9; Mismatches 17; Indels 20; Gaps 2;

QY 33 ADFWLSLCTADMSLLEQSHSPSLYLQCLSQKLQKRGRTIPGSGITESKDMHFSSLGCIL 92
Db 28 SSFFFLYSTTDF-LCTRSHSCPDAY-----VTDKQPQVYAAGCVY 67
QY 93 L 93
Db 68 I 68

RESULT 4
US-09-295-028-26
/ Sequence 26, Application US/09295028
/ Patent No. 6277381
/ GENERAL INFORMATION:
/ APPLICANT: Reed, Steven G.
/ APPLICANT: Lodes, Michael J.
/ APPLICANT: Houghton, Raymond L.
/ APPLICANT: McNeill, Patricia D.
/ TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
/ FILE REFERENCE: 210121.439C4
/ CURRENT APPLICATION NUMBER: US/09/295,028
/ CURRENT FILING DATE: 1999-04-20
/ NUMBER OF SEQ ID NOS: 85
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 26
/ LENGTH: 89
/ TYPE: PRT
/ ORGANISM: Ehrlichia sp.
/ US-09-295-028-26

Query Match 11.5%; Score 57; DB 3; Length 89;
Best Local Similarity 24.6%; Pred. No. 6.7;
Matches 15; Conservative 9; Mismatches 17; Indels 20; Gaps 2;

QY 33 ADFWLSLCTADMSLLEQSHSPSLYLQCLSQKLQKRGRTIPGSGITESKDMHFSSLGCIL 92
Db 28 SSFFFLYSTTDF-LCTRSHSCPDAY-----VTDKQPQVYAAGCVY 67
QY 93 L 93
Db 68 I 68

RESULT 5
US-09-106-582-26
/ Sequence 26, Application US/09106582
/ Patent No. 6306402
/ GENERAL INFORMATION:
/ APPLICANT: Reed, Steven G.
/ APPLICANT: Lodes, Michael J.
/ APPLICANT: Houghton, Raymond
/ TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND
/ NUMBER OF SEQUENCES: 73
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: SEED and BERRY LLP
/ THERAPY

STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/106,582
FILING DATE: 29-JUN-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.439C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
TELEFAX: 206-682-6031
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 89 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Ehrlichia
US-09-106-582-26

Query Match 11.5%; Score 57; DB 3; Length 89;
Best Local Similarity 24.6%; Pred. No. 6.7;
Matches 15; Conservative 9; Mismatches 17; Indels 20; Gaps 2;

QY 33 ADFWLSCTADMSLLEQSHSPSLYLQCLSQKLRQERTIPGSGITESKDMHFSSLCIL 92
DB 28 SSFFFLYSTDF-LCTRSHSCPDAY-----VTDKAPQVFAAGCVY 67
QY 93 L 93
DB 68 I 68

RESULT 6
US-09-159-469-26
Sequence 26, Application US/09159469
Patent No. 6607728
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND
THERAPY OF EHRlichia INFECTION
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/159,469
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/106,582
FILING DATE: 29-JUN-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.439C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
TELEFAX: 206-682-6031
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 89 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Ehrlichia
US-09-159-469-26

Query Match 11.5%; Score 57; DB 4; Length 89;
Best Local Similarity 24.6%; Pred. No. 6.7;
Matches 15; Conservative 9; Mismatches 17; Indels 20; Gaps 2;

QY 33 ADFWLSCTADMSLLEQSHSPSLYLQCLSQKLRQERTIPGSGITESKDMHFSSLCIL 92
DB 28 SSFFFLYSTDF-LCTRSHSCPDAY-----VTDKAPQVFAAGCVY 67
QY 93 L 93
DB 68 I 68

RESULT 7
US-09-693-542-26
Sequence 26, Application US/09693542
Patent No. 6673356
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
AND TREATMENT OF EHRlichia INFECTION
FILE REFERENCE: 210121.439C6
CURRENT APPLICATION NUMBER: US/09/693,542
CURRENT FILING DATE: 2000-10-20
NUMBER OF SEQ ID NOS: 89
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 26
LENGTH: 89
TYPE: PRT
ORGANISM: Ehrlichia sp.
US-09-693-542-26

Query Match 11.5%; Score 57; DB 4; Length 89;
Best Local Similarity 24.6%; Pred. No. 6.7;
Matches 15; Conservative 9; Mismatches 17; Indels 20; Gaps 2;
QY 33 ADFWLSCTADMSLLEQSHSPSLYLQCLSQKLRQERTIPGSGITESKDMHFSSLCIL 92
DB 28 SSFFFLYSTDF-LCTRSHSCPDAY-----VTDKAPQVFAAGCVY 67
QY 93 L 93
DB 68 I 68

RESULT 8
US-09-248-796A-25093
Sequence 25093, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:

```
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 25093
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-25093

Query Match      11.2%; Score 55.5; DB 4; Length 64;
Best Local Similarity 40.5%; Pred. No. 6.7;
Matches 15; Conservative 5; Mismatches 12; Indels 5; Gaps 2;

QY 6 LLEVDGPAKMNVEFKAQKRGGLCT---VHREADFFWS 38
Db 13 LLEFDKKIKNKIKYKQ-TCTLOQLVHTENDSLWS 48

RESULT 9
US-09-621-976-7393
; Sequence 7393, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSEI.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 7393
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: UNSURE
; LOCATION: 4
; OTHER INFORMATION: Xaa = Ala,Asp,Gly,Val
US-09-621-976-7393

Query Match      10.4%; Score 51.5; DB 4; Length 75;
Best Local Similarity 25.4%; Pred. No. 29;
Matches 15; Conservative 12; Mismatches 23; Indels 9; Gaps 1;

QY 12 PAKMNVEFKAQKRGGLCTVHRE-----ADFFWSLCTADMSLLEQSHSPSYLQCL 61
Db 17 PLPQHIFFOSSARNLCAENRRKAQGAALPTGTFHSSQASSAKAGREETHSPNPYDQGL 75

RESULT 10
US-09-187-789-52
; Sequence 52, Application US/09187789
; Patent No. 6340740
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING
; FILE REFERENCE: 480140.434C1
; CURRENT APPLICATION NUMBER: US/09/187,789
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0

; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING
; FILE REFERENCE: 480140.434D1
; CURRENT APPLICATION NUMBER: US/09/989,903
; CURRENT FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 52
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-989-903-52

Query Match      10.1%; Score 50; DB 4; Length 47;
Best Local Similarity 33.3%; Pred. No. 24;
Matches 12; Conservative 7; Mismatches 17; Indels 0; Gaps 0;

QY 32 EADFFWSLCTADMSLLEQSHSPSYLQCLSQKLKQ 67
Db 10 EADFLGMATVLMCVSYRDPVNGTWIQLCSLRE 45

RESULT 11
US-09-139-600-47
; Sequence 47, Application US/09139600
; Patent No. 6432628
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING
; FILE REFERENCE: 480140.434
; CURRENT APPLICATION NUMBER: US/09/139,600
; CURRENT FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-139-600-47

Query Match      10.1%; Score 50; DB 4; Length 47;
Best Local Similarity 33.3%; Pred. No. 24;
Matches 12; Conservative 7; Mismatches 17; Indels 0; Gaps 0;

QY 32 EADFFWSLCTADMSLLEQSHSPSYLQCLSQKLKQ 67
Db 10 EADFLGMATVLMCVSYRDPVNGTWIQLCSLRE 45

RESULT 12
US-09-989-903-52
; Sequence 52, Application US/09989903
; Patent No. 6797812
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING
; FILE REFERENCE: 480140.434D1
; CURRENT APPLICATION NUMBER: US/09/989,903
; CURRENT FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 52
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-989-903-52

Query Match      10.1%; Score 50; DB 4; Length 47;
Best Local Similarity 33.3%; Pred. No. 24;
Matches 12; Conservative 7; Mismatches 17; Indels 0; Gaps 0;

QY 32 EADFFWSLCTADMSLLEQSHSPSYLQCLSQKLKQ 67
Db 10 EADFLGMATVLMCVSYRDPVNGTWIQLCSLRE 45
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RESULT 13
US-09-583-110-4281
; Sequence 4281, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 4281
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-4281

Query Match 10.1%; Score 50; DB 4; Length 88;
Best Local Similarity 29.3%; Pred. No. 58;
Matches 22; Conservative 9; Mismatches 22; Indels 22; Gaps 4;

QY 11 GPAMKNVEFKAKR-----GLCTVHREADFFWS-----LCTADMSLLEQSHSPS 55
DB 3 GDGMKEFQERKQFSLRPYAGACSVLLGTSLFFAGMGAPVQDTETSSALISSH---- 58

QY 56 LYL--OCLSKLRQE 68
DB 59 -YLDEQDLSEKLKSE 72

RESULT 14
US-09-107-433-3932
; Sequence 3932, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007

TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 3932:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 88 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...88
; SEQUENCE DESCRIPTION: SEQ ID NO: 3932:
US-09-107-433-3932

Query Match 10.1%; Score 50; DB 4; Length 88;
Best Local Similarity 29.3%; Pred. No. 58;
Matches 22; Conservative 9; Mismatches 22; Indels 22; Gaps 4;

QY 11 GPAMKNVEFKAKR-----GLCTVHREADFFWS-----LCTADMSLLEQSHSPS 55
DB 3 GDGMKEFQERKQFSLRPYAGACSVLLGTSLFFAGMGAPVQDTETSSALISSH---- 58

QY 56 LYL--OCLSKLRQE 68
DB 59 -YLDEQDLSEKLKSE 72

RESULT 15
US-09-107-532A-4733
; Sequence 4733, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 4733:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 96 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:

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; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...96
; SEQUENCE DESCRIPTION: SEQ ID NO: 4733:
US-09-107-532A-4733

Query Match      10.1%; Score 50; DB 4; Length 96;
Best Local Similarity 23.2%; Pred. NO. 65;
Matches 13; Conservative 15; Mismatches 24; Indels 4; Gaps 1;

QY      14 MKNVEFKAKRGICTVHRE----ADFFWSLCTADMSLLEQSHSPSLYLQCLSQKL 65
      ::::| | :| | :| | | : : : : | : | :| :| |
Db      2 VRHMEIKKEKNRLALFNDEQQBIGEMTWS DAGFDIMIIDHTFVDPAYRGQKLAEXL 57

Search completed: June 20, 2005, 14:04:44
Job time : 44 secs
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